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SEQUENCING

(A)

Tue Jul 17 14:07:15 2001 [BLASTN 2.1.3 [Apr-1-2001], NCBI]
Repeats masked. (summary below)
/home/ruby/va/Molbio/carpenda/temp1/ss.DNA37151 (3679 bp)

Sequences producing High-scoring Segment Pairs:

		Frame	Score	Match	Pct	E-value
1	P_AAF72414 Human PRO293 cDNA.	+	3679	3679	100	
2	P_AAX52256 Protein PRO293 cDNA clone DNA37151-1193.	+	3679	3679	100	
3	AC021462 Homo sapiens clone RP11-276C1, WORKING D	+	3658	3670	100	
4	AL512306 Homo sapiens chromosome 1 clone RP11-430	-	3658	3670	100	
5	NM_006338 Homo sapiens glioma amplified on chromos	+	3002	3017	100	0.0
6	AF030435 Homo sapiens glioma amplified on chromos	+	3002	3017	100	0.0

>1 P_AAF72414 Human PRO293 cDNA. (3679 bp) [1 seg]

Score = 3679 (7293 bits), Expect = 0.0

Identities = 3679/3679 (100%), at 1,1-3679,3679, Strand +/+

DNA37151 1 AAGGAGGCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTCTGGG

P_AAF72414 1 AAGGAGGCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTCTGGG

DNA37151 61 CTCAGAAGGACTCTGAAGATAACAATAATTCAAGCCATCCACTCTCCTCCCTCCCAA

P_AAF72414 61 CTCAGAAGGACTCTGAAGATAACAATAATTCAAGCCATCCACTCTCCTCCCTCCCAA

DNA37151 121 CACACATGTGCATGTACACACACATACACACATACACCTTCCTCTCCTCACTGAA

P_AAF72414 121 CACACATGTGCATGTACACACACATACACACATACACCTTCCTCTCCTCACTGAA

DNA37151 181 GACTCACAGTCACTCACTCTGTGAGCAGGTCA TAGAAAAGGACACTAAAGCCTTAAGGAC

P_AAF72414 181 GACTCACAGTCACTCACTCTGTGAGCAGGTCA TAGAAAAGGACACTAAAGCCTTAAGGAC

DNA37151 241 AGGCCTGCCATTACCTCTGCAGCTCCTTGGCTTGTGAGTCAAAAAACATGGGAGGGGG

P_AAF72414 241 AGGCCTGCCATTACCTCTGCAGCTCCTTGGCTTGTGAGTCAAAAAACATGGGAGGGGG

DNA37151 301 CCAGGCACGGTGACTCACACCTGTAATCCAGCATTTGGGAGACCGAGGGTGAGCAGATC

P_AAF72414 301 CCAGGCACGGTGACTCACACCTGTAATCCAGCATTTGGGAGACCGAGGGTGAGCAGATC

DNA37151 361 ACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGGAGAAACCCCCATCTCTACTA

P_AAF72414 361 ACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGGAGAAACCCCCATCTCTACTA

DNA37151 421 AAAATACAAAAATTAGCCAGGAGTGGTGGCAGGTGCCTGTAATCCCAGCTACTCAGGTGG

P_AAF72414 421 AAAATACAAAAATTAGCCAGGAGTGGTGGCAGGTGCCTGTAATCCCAGCTACTCAGGTGG

DNA37151 481 CTGAGCCAGGAGAATCGCTTGAATCCAGGAGGCGGGAGGATGCAGTCAGCTGAGTCACCG

P_AAF72414 481 CTGAGCCAGGAGAATCGCTTGAATCCAGGAGGCGGGAGGATGCAGTCAGCTGAGTCACCG

DNA37151 541 CTGCACTCCAGCCTGGGTGACAGAATGAGACTCTGCTCAAACAAACAAACACGGGAGGA

P_AAF72414 541 CTGCACTCCAGCCTGGGTGACAGAATGAGACTCTGCTCAAACAAACAAACACGGGAGGA

DNA37151 601 GGGGTAGATACTGCTTCTGCAACCTCCTTAACCTGCATCCTCTTCCAGGGCTGC

P_AAF72414 601 GGGGTAGATACTGCTTCTGCAACCTCCTTAACCTGCATCCTCTTCCAGGGCTGC

DNA37151 661 CCCTGATGGGCCTGGCAATGACTGAGCAGGCCAGCCCCAGAGGAAGAGAAGG

P_AAF72414 661 CCCTGATGGGCCTGGCAATGACTGAGCAGGCCAGCCCCAGAGGAAGAGAAGG

BLAST RESULTS A-1

BLAST RESULTS A-2

DNA37151	721	CATATTGAGGAGGGCAAGAAGTGACGCCCGGTGAGAATGACTGCCCTGGGAGGGTGGTT *****
P_AAF72414	721	CATATTGAGGAGGGCAAGAAGTGACGCCCGGTGAGAATGACTGCCCTGGGAGGGTGGTT *****
DNA37151	781	CCTTGGGCCCTGGCAGGGTTGCTGACCCCTAACCTGCAAAACACAAAGAGCAGGACTCCA *****
P_AAF72414	781	CCTTGGGCCCTGGCAGGGTTGCTGACCCCTAACCTGCAAAACACAAAGAGCAGGACTCCA *****
DNA37151	841	GACTCTCCTGTGAATGGTCCCTGCCCTGCAGCTCCACCATGAGGCTTCTCGTGGCCC *****
P_AAF72414	841	GACTCTCCTGTGAATGGTCCCTGCCCTGCAGCTCCACCATGAGGCTTCTCGTGGCCC *****
DNA37151	901	ACTCTTGCTAGCTTGGTGGCTGGTGCCTGCCACTGCCACTGTGCCGTGGTACCCGGCATGT *****
P_AAF72414	901	ACTCTTGCTAGCTTGGTGGCTGGTGCCTGCCACTGCCACTGTGCCGTGGTACCCGGCATGT *****
DNA37151	961	TCCCTGCCCCCTCAGTGTGCCTGCCAGATCCGGCCCTGGTATACGCCCGTCGTCC *****
P_AAF72414	961	TCCCTGCCCCCTCAGTGTGCCTGCCAGATCCGGCCCTGGTATACGCCCGTCGTCC *****
DNA37151	1021	CCCGCAGGCTACCACTGTGGACTGCAATGACCTATTCCGTACGGCAGTCCCCCGGC *****
P_AAF72414	1021	CCCGCAGGCTACCACTGTGGACTGCAATGACCTATTCCGTACGGCAGTCCCCCGGC *****
DNA37151	1081	CCCCGCAGGCACACAGACCCCTGCTCCTGCAGAGCAACAGCATTGTCCGTGGACCAGAG *****
P_AAF72414	1081	CCCCGCAGGCACACAGACCCCTGCTCCTGCAGAGCAACAGCATTGTCCGTGGACCAGAG *****
DNA37151	1141	TGAGCTGGCTACCTGGCCAATCTCACAGAGCTGGACCTGTCCAGAACAGCTTTCGGA *****
P_AAF72414	1141	TGAGCTGGCTACCTGGCCAATCTCACAGAGCTGGACCTGTCCAGAACAGCTTTCGGA *****
DNA37151	1201	TGCCCGAGACTGTGATTCCATGCCCTGCCAGCTGCTGAGCCTGCACCTAGAGGAGAA *****
P_AAF72414	1201	TGCCCGAGACTGTGATTCCATGCCCTGCCAGCTGCTGAGCCTGCACCTAGAGGAGAA *****
DNA37151	1261	CCAGCTGACCCGGCTGGAGGACCAAGCTTGCAAGGGCTGCCAGCCTACAGGAAC *****
P_AAF72414	1261	CCAGCTGACCCGGCTGGAGGACCAAGCTTGCAAGGGCTGCCAGCCTACAGGAAC *****
DNA37151	1321	TCTCAACCACAACCAGCTACCGCATGCCCTGCCAGGGCTTCTGGCCTCAGCAAC *****
P_AAF72414	1321	TCTCAACCACAACCAGCTACCGCATGCCCTGCCAGGGCTTCTGGCCTCAGCAAC *****
DNA37151	1381	GCTGCGGCTGCACCTCAACTCCAACCTCTGAGGGCATTGACAGCCGCTGGTTGA *****
P_AAF72414	1381	GCTGCGGCTGCACCTCAACTCCAACCTCTGAGGGCATTGACAGCCGCTGGTTGA *****
DNA37151	1441	GCTGCCAACCTGGAGATACTCATGATTGGCGCAACAAAGGTAGATGCCATCCTGG *****
P_AAF72414	1441	GCTGCCAACCTGGAGATACTCATGATTGGCGCAACAAAGGTAGATGCCATCCTGG *****
DNA37151	1501	GAACTTCCGGCCCTGGCCAACCTGCGTAGCCTGGTCTAGCAGGCATGAAC *****
P_AAF72414	1501	GAACTTCCGGCCCTGGCCAACCTGCGTAGCCTGGTCTAGCAGGCATGAAC *****
DNA37151	1561	GATCTCCGACTATGCCCTGGAGGGCTGCAAAGCCTGGAGAGCCTCTCCTTATG *****
P_AAF72414	1561	GATCTCCGACTATGCCCTGGAGGGCTGCAAAGCCTGGAGAGCCTCTCCTTATG *****
DNA37151	1621	CCAGCTGGCCCGGGTGCCCAGGCAGGCACTGGAACAGGTGCCCGGGCTCAAG *****
P_AAF72414	1621	CCAGCTGGCCCGGGTGCCCAGGCAGGCACTGGAACAGGTGCCCGGGCTCAAG *****

BURST RESULTS A-3

DNA37151	1681	CCTCAACAAGAACCCGCTCCAGCGGGTAGGGCGGGGGACTTGCACATGCTGCACCT
P_AAF72414	1681	*****
DNA37151	1741	TAAGGAGCTGGGACTGAACAACATGGAGGAGCTGGCTCCATCGACAAGTTGCCCTGGT
P_AAF72414	1741	*****
DNA37151	1801	GAACCTCCCCGAGCTGACCAAGCTGGACATCACCAATAACCCACGGCTGTCCATCCA
P_AAF72414	1801	*****
DNA37151	1861	CCCCCGGCCCTCACCACCTGCCCCAGATGGAGACCCCTCATGCTCAACAACAAACGCTCT
P_AAF72414	1861	*****
DNA37151	1921	CAGTGCCTTGACCAAGCAGACGGTGGAGTCCTGCCAACCTGCAGGAGGTAGGTCTCCA
P_AAF72414	1921	*****
DNA37151	1981	CGGCAACCCCATTCCGCTGTGACTGTGTCATCCGCTGGCCAATGCCACGGCACCCGTGT
P_AAF72414	1981	*****
DNA37151	2041	CCGCTTCATCGAGCCGAATCCACCCCTGTGTGCGGAGCCTCCGGACCTCCAGCGCCTCCC
P_AAF72414	2041	*****
DNA37151	2101	GGTCCGTGAGGTGCCCTCCGGGAGATGACGGACCCTGTTGCCCTCATCTCCCCACG
P_AAF72414	2101	*****
DNA37151	2161	AAGCTTCCCCCAAGCCTCCAGGTAGCCAGTGGAGAGAGCATGGTGCATTGCCGGG
P_AAF72414	2161	*****
DNA37151	2221	ACTGGCCGAACCGAACCCGAGATCTACTGGGTCACTCCAGCTGGCTTCGACTGACACC
P_AAF72414	2221	*****
DNA37151	2281	TGCCCATGCAGGCAGGGAGGTACCGGGTGTACCCCGAGGGGACCCCTGGAGCTGCGGAGGGT
P_AAF72414	2281	*****
DNA37151	2341	GACAGCAGAAGAGGCAGGGCTATACACCTGTGTGGCCAGAACCTGGTGGGGCTGACAC
P_AAF72414	2341	*****
DNA37151	2401	TAAGACGGTTAGTGTGGTTGTGGCCGTGCTCTCCAGCCAGGCAGGGACGAAGGACA
P_AAF72414	2401	*****
DNA37151	2461	GGGGCTGGAGCTCCGGGTGCAGGAGACCCACCCCTATCACATCCTGCTATCTGGGTAC
P_AAF72414	2461	*****
DNA37151	2521	CCCACCCAACACAGTGTCCACCAACCTCACCTGGTCCAGTGCCTCCTCCCTCGGGGCCA
P_AAF72414	2521	*****
DNA37151	2581	GGGGGCCACAGCTCTGGCCCGCCTGCCTGGGAACCCACAGCTACAACATTACCCGCCT
P_AAF72414	2581	*****

BLAST RESULTS A-4

DNA37151	2641	CCTTCAGGCCACGGAGTACTGGGCCTGCCCTGCAAGTGGCCTTGCTGATGCCAACACCCA *****
P_AAF72414	2641	CCTTCAGGCCACGGAGTACTGGGCCTGCCCTGCAAGTGGCCTTGCTGATGCCAACACCCA *****
DNA37151	2701	GTTGGCTTGTATGGCCAGGACAAAGAGGCCACTTCTGCCACAGAGCCTTAGGGGA *****
P_AAF72414	2701	GTTGGCTTGTATGGCCAGGACAAAGAGGCCACTTCTGCCACAGAGCCTTAGGGGA *****
DNA37151	2761	TCGTCCTGGCCTCATGCCATTGGCTCTGGCTCTCGCTGCCCTCTGGCAGCTGGCTAGC *****
P_AAF72414	2761	TCGTCCTGGCCTCATGCCATTGGCTCTGGCTCTCGCTGCCCTCTGGCAGCTGGCTAGC *****
DNA37151	2821	GGCCCACCTTGGCACAGGCCAACCCAGGAAGGGTGTGGTGGGAGGCGGCCCTCC *****
P_AAF72414	2821	GGCCCACCTTGGCACAGGCCAACCCAGGAAGGGTGTGGTGGGAGGCGGCCCTCC *****
DNA37151	2881	AGCCTGGCTTCTGGGCTGGAGTGCCCTCTGTCCGGTTGTGTCTGCTCCCCCTGT *****
P_AAF72414	2881	AGCCTGGCTTCTGGGCTGGAGTGCCCTCTGTCCGGTTGTGTCTGCTCCCCCTGT *****
DNA37151	2941	CCTGCCCTGGAATCCAGGGAGGAAGCTGCCAGATCCTCAGAAGGGAGACACTGTTGCC *****
P_AAF72414	2941	CCTGCCCTGGAATCCAGGGAGGAAGCTGCCAGATCCTCAGAAGGGAGACACTGTTGCC *****
DNA37151	3001	ACCATTGTCTCAAATTCTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGA *****
P_AAF72414	3001	ACCATTGTCTCAAATTCTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGA *****
DNA37151	3061	CTACTTTTACCAAAAGAGAACAGCAGTCTGGGCCAGATGCCCTGCCAGGAAAGGGACATGG *****
P_AAF72414	3061	CTACTTTTACCAAAAGAGAACAGCAGTCTGGGCCAGATGCCCTGCCAGGAAAGGGACATGG *****
DNA37151	3121	ACCCACGTGCTTGAGGCCCTGGCAGCTGGCCAAGACAGATGGGCTTGTGGCCCTGGG *****
P_AAF72414	3121	ACCCACGTGCTTGAGGCCCTGGCAGCTGGCCAAGACAGATGGGCTTGTGGCCCTGGG *****
DNA37151	3181	GTGCTTCTGCAGCCTTGAAAAGTTGCCATTACCTCTAGGGTCACCTCTGCTGCCATT *****
P_AAF72414	3181	GTGCTTCTGCAGCCTTGAAAAGTTGCCATTACCTCTAGGGTCACCTCTGCTGCCATT *****
DNA37151	3241	TGAGGAACATCTCAAGGAACAGGAGGGACTTGGTAGAGCCTCTGCCCTCCCATCT *****
P_AAF72414	3241	TGAGGAACATCTCAAGGAACAGGAGGGACTTGGTAGAGCCTCTGCCCTCCCATCT *****
DNA37151	3301	CTCTCTGCCAGAGGCTCCTGGGCCCTGGCTGGCTGTCCCCTACCTGTGTCCTGGGCTG *****
P_AAF72414	3301	CTCTCTGCCAGAGGCTCCTGGGCCCTGGCTGGCTGTCCCCTACCTGTGTCCTGGGCTG *****
DNA37151	3361	CACCCCTCCTCTTCTCTTCTGTACAGTCTCAGTTGCTCTTGCTGCCTGG *****
P_AAF72414	3361	CACCCCTCCTCTTCTCTGTACAGTCTCAGTTGCTCTTGCTGCCTGG *****
DNA37151	3421	CAAGGGCTGAAGGAGGCCACTCCATCTCACCTCGGGGGCTGCCCTCAATGTGGGAGTGA *****
P_AAF72414	3421	CAAGGGCTGAAGGAGGCCACTCCATCTCACCTCGGGGGCTGCCCTCAATGTGGGAGTGA *****
DNA37151	3481	CCCCAGCCAGATCTGAAGGACATTGGAGAGGAATGCCAGGAACGCCATCTCAGCA *****
P_AAF72414	3481	CCCCAGCCAGATCTGAAGGACATTGGAGAGGAATGCCAGGAACGCCATCTCAGCA *****
DNA37151	3541	GCCTGGCTCGGCATTCCGAAGCTGACTTCTATAAGGCAATTGTACCTTGAGGAA *****
P_AAF72414	3541	GCCTGGCTCGGCATTCCGAAGCTGACTTCTATAAGGCAATTGTACCTTGAGGAA *****

BLAST RESULTS A-5

DNA37151	3601	ATGTGTCACCTCCCCAACCGATTCACTCTTCTCCTGTTGTAAAAAATAAAAATA *****
P_AAF72414	3601	ATGTGTCACCTCCCCAACCGATTCACTCTTCTCCTGTTGTAAAAAATAAAAATA *****
DNA37151	3661	AATAATAACAATAAAAAAA *****
P_AAF72414	3661	AATAATAACAATAAAAAAA *****
>2 P_AAX52256 Protein PRO293 cDNA clone DNA37151-1193. DNA, PAT 25-JUN-1999 (3679 bp) [1 seg]		
Score = 3679 (7293 bits), Expect = 0.0		
Identities = 3679/3679 (100%), at 1,1-3679,3679, Strand +/-		
DNA37151	1	AAGGAGGCCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTCTGGG *****
P_AAX52256	1	AAGGAGGCCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTCTGGG *****
DNA37151	61	CTCAGAAGGACTCTGAAGATAACAATAATTTCAGCCCATCCACTCTCCTCCCTCCCAA *****
P_AAX52256	61	CTCAGAAGGACTCTGAAGATAACAATAATTTCAGCCCATCCACTCTCCTCCCTCCCAA *****
DNA37151	121	CACACATGTGCATGTACACACACACATACACACATACACCTTCCTCTCCTCACTGAA *****
P_AAX52256	121	CACACATGTGCATGTACACACACACATACACACATACACCTTCCTCTCCTCACTGAA *****
DNA37151	181	GACTCACAGTCACTCACTCTGTGAGCAGGTATAGAAAAGGACACTAAAGCCTTAAGGAC *****
P_AAX52256	181	GACTCACAGTCACTCACTCTGTGAGCAGGTATAGAAAAGGACACTAAAGCCTTAAGGAC *****
DNA37151	241	AGGCCTGCCATTACCTCTGCAGCTCTTGAGTCAAAAAACATGGGAGGGGG *****
P_AAX52256	241	AGGCCTGCCATTACCTCTGCAGCTCTTGAGTCAAAAAACATGGGAGGGGG *****
DNA37151	301	CCAGGCACGGTGACTCACACCTGTAATCCCAGCATTTGGGAGACCGAGGTGAGCAGATC *****
P_AAX52256	301	CCAGGCACGGTGACTCACACCTGTAATCCCAGCATTTGGGAGACCGAGGTGAGCAGATC *****
DNA37151	361	ACTTGAGGTCAAGGAGTTCGAGACCAGCCTGGCCAACATGGGAGAAACCCCATCTCTACTA *****
P_AAX52256	361	ACTTGAGGTCAAGGAGTTCGAGACCAGCCTGGCCAACATGGGAGAAACCCCATCTCTACTA *****
DNA37151	421	AAAATACAAAATTAGCCAGGAGTGGTGGCAGGTGCCTGTAATCCCAGCTACTCAGGTGG *****
P_AAX52256	421	AAAATACAAAATTAGCCAGGAGTGGTGGCAGGTGCCTGTAATCCCAGCTACTCAGGTGG *****
DNA37151	481	CTGAGCCAGGAGAACATCGCTTGAATCCAGGAGGCGGAGGATGCAGTCAGCTGAGTCACCG *****
P_AAX52256	481	CTGAGCCAGGAGAACATCGCTTGAATCCAGGAGGCGGAGGATGCAGTCAGCTGAGTCACCG *****
DNA37151	541	CTGCACTCCAGCCTGGGTGACAGAACATGGAGACTCTGCTCAAACAAACAAACACGGGAGGA *****
P_AAX52256	541	CTGCACTCCAGCCTGGGTGACAGAACATGGAGACTCTGCTCAAACAAACAAACACGGGAGGA *****
DNA37151	601	GGGGTAGATACTGCTCTGCAACCTCTTAACCTGCATCCTCTTCCAGGGCTGC *****
P_AAX52256	601	GGGGTAGATACTGCTCTGCAACCTCTTAACCTGCATCCTCTTCCAGGGCTGC *****
DNA37151	661	CCCTGATGGGGCTGGCAATGACTGAGCAGGCCAGCCCCAGAGGAAGAGAAGG *****
P_AAX52256	661	CCCTGATGGGGCTGGCAATGACTGAGCAGGCCAGCCCCAGAGGAAGAGAAGG *****
DNA37151	721	CATATTGAGGAGGGCAAGAAGTGAACGCCGGTGTAGAATGACTGCCCTGGGAGGGTGGTT *****

BLAST RESULTS ALL

P_AAX52256	721	CATATTGAGGAGGGCAAGAAGTGACGCCCGGTGAGAATGACTGCCCTGGGAGGGTGGTT
DNA37151	781	CCTTGGGCCTGGCAGGGTTGCTGACCCCTAACCTGCAAAACACAAAGAGCAGGACTCCA *****
P_AAX52256	781	CCTTGGGCCTGGCAGGGTTGCTGACCCCTAACCTGCAAAACACAAAGAGCAGGACTCCA *****
DNA37151	841	GACTCTCCTTGTGAATGGTCCCCTGCCCTGCAGCTCCACCATGAGGCTTCTCGTGGCCCC *****
P_AAX52256	841	GACTCTCCTTGTGAATGGTCCCCTGCCCTGCAGCTCCACCATGAGGCTTCTCGTGGCCCC *****
DNA37151	901	ACTCTTGCTAGCTTGGGTGGCTGGTGCCACTGCCACTGTGCCGTGGTACCCCTGGCATGT *****
P_AAX52256	901	ACTCTTGCTAGCTTGGGTGGCTGGTGCCACTGCCACTGTGCCGTGGTACCCCTGGCATGT *****
DNA37151	961	TCCCTGCCCTTCAGTGTGCCTGCCAGATCCGGCCCTGGTATACGCCCGCTCGTCCTA *****
P_AAX52256	961	TCCCTGCCCTTCAGTGTGCCTGCCAGATCCGGCCCTGGTATACGCCCGCTCGTCCTA *****
DNA37151	1021	CCCGGAGGCTACCACTGTGGACTGCAATGACCTATTCCCTGACGGCAGTCCCCCGGCACT *****
P_AAX52256	1021	CCCGGAGGCTACCACTGTGGACTGCAATGACCTATTCCCTGACGGCAGTCCCCCGGCACT *****
DNA37151	1081	CCCCGAGGCACACAGACCCCTGCTCCTGCAGAGCACAGCATTGTCCGTGGACCAAGAG *****
P_AAX52256	1081	CCCCGAGGCACACAGACCCCTGCTCCTGCAGAGCACAGCATTGTCCGTGGACCAAGAG *****
DNA37151	1141	TGAGCTGGCTACCTGGCAATCTCACAGAGCTGGACCTGTCCAGAACAGCTTTCGGA *****
P_AAX52256	1141	TGAGCTGGCTACCTGGCAATCTCACAGAGCTGGACCTGTCCAGAACAGCTTTCGGA *****
DNA37151	1201	TGCCCGAGACTGTGATTCCATGCCCTGCCAGCTGCTGAGGCTGCACCTAGAGGAGAA *****
P_AAX52256	1201	TGCCCGAGACTGTGATTCCATGCCCTGCCAGCTGCTGAGGCTGCACCTAGAGGAGAA *****
DNA37151	1261	CCAGCTGACCGGGCTGGAGGACCAAGCTTGCAAGGGCTGGCAGCCTACAGGAACCTCA *****
P_AAX52256	1261	CCAGCTGACCGGGCTGGAGGACCAAGCTTGCAAGGGCTGGCAGCCTACAGGAACCTCA *****
DNA37151	1321	TCTCAACCACAACCAGCTAACCGCATGCCCTCCCCAGGGCTTTCTGGCCTCAGCAACTT *****
P_AAX52256	1321	TCTCAACCACAACCAGCTAACCGCATGCCCTCCCCAGGGCTTTCTGGCCTCAGCAACTT *****
DNA37151	1381	GCTGCGGCTGCACCTCAACTCCAACCTCTGAGGGCATTGACAGCCGCTGGTTGAAAT *****
P_AAX52256	1381	GCTGCGGCTGCACCTCAACTCCAACCTCTGAGGGCATTGACAGCCGCTGGTTGAAAT *****
DNA37151	1441	GCTGCCCAACTTGGAGATACTCATGATTGGCGCAACAAGGTAGATGCCATCCTGGACAT *****
P_AAX52256	1441	GCTGCCCAACTTGGAGATACTCATGATTGGCGCAACAAGGTAGATGCCATCCTGGACAT *****
DNA37151	1501	GAACCTCCGGCCCTGGCAAACCTGCGTAGCCTGGCTAGCAGGCATGAACCTGCGGGA *****
P_AAX52256	1501	GAACCTCCGGCCCTGGCAAACCTGCGTAGCCTGGCTAGCAGGCATGAACCTGCGGGA *****
DNA37151	1561	GATCTCCGACTATGCCCTGGAGGGCTGCAAAGCCTGGAGAGCCTCTCCTATGACAA *****
P_AAX52256	1561	GATCTCCGACTATGCCCTGGAGGGCTGCAAAGCCTGGAGAGCCTCTCCTATGACAA *****
DNA37151	1621	CCAGCTGGCCCGGGTGCCAGGCGGGACTGGAACAGGTGCCGGCTCAAGTCCCTAGA *****
P_AAX52256	1621	CCAGCTGGCCCGGGTGCCAGGCGGGACTGGAACAGGTGCCGGCTCAAGTCCCTAGA *****
DNA37151	1681	CCTCAACAAGAACCCGCTCCAGCGGGTAGGGCGGGGACTTGCAACATGCTGCACCT *****

BLAST RESULTS A-T

P_AAX52256 1681 CCTCAACAAGAACCGCTCCAGCGGTAGGGCGGGGACTTGCCAACATGCTGCACCT
DNA37151 1741 TAAGGAGCTGGGACTGAACAAACATGGAGGAGCTGGTCTCCATCGACAAGTTGCCCTGGT

P_AAX52256 1741 TAAGGAGCTGGGACTGAACAAACATGGAGGAGCTGGTCTCCATCGACAAGTTGCCCTGGT
DNA37151 1801 GAACCTCCCCGAGCTGACCAAGCTGGACATCACCAATAACCCACGGCTGTCCTTCATCCA

P_AAX52256 1801 GAACCTCCCCGAGCTGACCAAGCTGGACATCACCAATAACCCACGGCTGTCCTTCATCCA
DNA37151 1861 CCCCCGCGCCTTCCACCACCTGCCCCAGATGGAGACCCCTCATGCTCAACAAACAACGCTCT

P_AAX52256 1861 CCCCCGCGCCTTCCACCACCTGCCCCAGATGGAGACCCCTCATGCTCAACAAACAACGCTCT
DNA37151 1921 CAGTGCCTTGCACCAGCAGACGGTGGAGTCCCTGCCAACCTGCAGGAGGTAGGTCTCCA

P_AAX52256 1921 CAGTGCCTTGCACCAGCAGACGGTGGAGTCCCTGCCAACCTGCAGGAGGTAGGTCTCCA
DNA37151 1981 CGGCAACCCCATCCGCTGTGACTGTGTCATCCGCTGGGCAATGCCACGGCACCCGTGT

P_AAX52256 1981 CGGCAACCCCATCCGCTGTGACTGTGTCATCCGCTGGGCAATGCCACGGCACCCGTGT
DNA37151 2041 CCGCTTCATCGAGCGCAATCCACCCCTGTGCGGAGCCTCCGGACCTCCAGCGCCTCCC

P_AAX52256 2041 CCGCTTCATCGAGCGCAATCCACCCCTGTGCGGAGCCTCCGGACCTCCAGCGCCTCCC
DNA37151 2101 GGTCCGTAGGTGCCCTCCGGGAGATGACGGACCACTGTTGCCCTCATCTCCCCACG

P_AAX52256 2101 GGTCCGTAGGTGCCCTCCGGGAGATGACGGACCACTGTTGCCCTCATCTCCCCACG
DNA37151 2161 AAGCTTCCCCCAAGCCTCCAGGTAGCCAGTGGAGAGAGCATGGTGCTGCATTGCCGGGC

P_AAX52256 2161 AAGCTTCCCCCAAGCCTCCAGGTAGCCAGTGGAGAGAGCATGGTGCTGCATTGCCGGGC
DNA37151 2221 ACTGGCGAACCGAACCCGAGATCTACTGGGTCACTCCAGCTGGCTTCGACTGACACC

P_AAX52256 2221 ACTGGCGAACCGAACCCGAGATCTACTGGGTCACTCCAGCTGGCTTCGACTGACACC
DNA37151 2281 TGCCCATGCAGGCAGGGAGGTACCGGGTGTACCCCGAGGGGACCTGGAGCTGCGGAGGGT

P_AAX52256 2281 TGCCCATGCAGGCAGGGAGGTACCGGGTGTACCCCGAGGGGACCTGGAGCTGCGGAGGGT
DNA37151 2341 GACAGCAGAAGAGGCAGGGCTATAACACCTGTGTTGGCCAGAACCTGGTGGGGCTGACAC

P_AAX52256 2341 GACAGCAGAAGAGGCAGGGCTATAACACCTGTGTTGGCCAGAACCTGGTGGGGCTGACAC
DNA37151 2401 TAAGACGGTTAGTGTGGTTGTGGCCGTGCTCTCCCTCCAGCCAGGCAGGGACGAAGGACA

P_AAX52256 2401 TAAGACGGTTAGTGTGGTTGTGGCCGTGCTCTCCAGCCAGGCAGGGACGAAGGACA
DNA37151 2461 GGGGCTGGAGCTCCGGGTGCAGGAGACCCACCCCTATCACATCCTGCTATCTGGTCAC

P_AAX52256 2461 GGGGCTGGAGCTCCGGGTGCAGGAGACCCACCCCTATCACATCCTGCTATCTGGTCAC
DNA37151 2521 CCCACCCAAACACAGTGTCCACCAACCTCACCTGGTCAGTGCCTCCTCCCTCCGGGGCCA

P_AAX52256 2521 CCCACCCAAACACAGTGTCCACCAACCTCACCTGGTCAGTGCCTCCTCCCTCCGGGGCCA
DNA37151 2581 GGGGGCCACAGCTCTGGCCCGCCTGCCTCGGGAACCCACAGCTACAACATTACCCGCCT

P_AAX52256 2581 GGGGGCCACAGCTCTGGCCCGCCTGCCTCGGGAACCCACAGCTACAACATTACCCGCCT
DNA37151 2641 CCTTCAGGCCACGGAGTACTGGGCCTGCCTGCAAGTGGCCTTGCTGATGCCACACCCA

BLAST RESULTS A9

P_AAX52256	2641	CCTTCAGGCCACGGACTACTGGGCCTGCCGTCAAGTGGCCTTGCTGATGCCAACACCCA
DNA37151	2701	GTTGGCTTGTATGGGCAGGACCAAAGAGGCCACTTCTGCCACAGAGCCTAGGGGA *****
P_AAX52256	2701	GTTGGCTTGTATGGGCAGGACCAAAGAGGCCACTTCTGCCACAGAGCCTAGGGGA
DNA37151	2761	TCGTCCTGGCTATTGCCATCCTGGCTCGCTGCCTCTCCCTGGCAGCTGGCTAGC *****
P_AAX52256	2761	TCGTCCTGGCTATTGCCATCCTGGCTCGCTGCCTCTCCCTGGCAGCTGGCTAGC
DNA37151	2821	GGCCCACCTTGGCACAGGCCAACCCAGGAAGGGTGTGGTGGGAGGCAGGCCTCTCCCTCC *****
P_AAX52256	2821	GGCCCACCTTGGCACAGGCCAACCCAGGAAGGGTGTGGTGGGAGGCAGGCCTCTCCCTCC
DNA37151	2881	AGCCTGGGCTTCTGGGCTGGAGTGCCTCTGTCCGGTTGTGTCTGCTCCCCCTCGT *****
P_AAX52256	2881	AGCCTGGGCTTCTGGGCTGGAGTGCCTCTGTCCGGTTGTGTCTGCTCCCCCTCGT
DNA37151	2941	CCTGCCCTGGAATCCAGGGAGGAAGCTGCCAGATCCTCAGAAGGGAGACACTGTTGCC *****
P_AAX52256	2941	CCTGCCCTGGAATCCAGGGAGGAAGCTGCCAGATCCTCAGAAGGGAGACACTGTTGCC
DNA37151	3001	ACCATTGTCTAAAATTCTTGAAGCTCAGCCTGTTCTCAGCACTAGAGAAATCACTAGGA *****
P_AAX52256	3001	ACCATTGTCTAAAATTCTTGAAGCTCAGCCTGTTCTCAGCACTAGAGAAATCACTAGGA
DNA37151	3061	CTACTTTTACCAAAAGAGAAGCAGTCTGGCCAGATGCCCTGCCAGGAAAGGGACATGG *****
P_AAX52256	3061	CTACTTTTACCAAAAGAGAAGCAGTCTGGCCAGATGCCCTGCCAGGAAAGGGACATGG
DNA37151	3121	ACCCACGTGCTTGAGGCCTGGCAGCTGGCCAAGACAGATGGGGTTGTGGCCCTGGGG *****
P_AAX52256	3121	ACCCACGTGCTTGAGGCCTGGCAGCTGGCCAAGACAGATGGGGTTGTGGCCCTGGGG
DNA37151	3181	GTGCTTCTGCAGCCTTGAAAAGTTGCCCTACCTCCTAGGGTCACCTCTGCTGCCATT *****
P_AAX52256	3181	GTGCTTCTGCAGCCTTGAAAAGTTGCCCTACCTCCTAGGGTCACCTCTGCTGCCATT
DNA37151	3241	TGAGGAACATCTCAAGGAACAGGAGGGACTTGGTAGAGCCTCCTGCCCTCCCATCTT *****
P_AAX52256	3241	TGAGGAACATCTCAAGGAACAGGAGGGACTTGGTAGAGCCTCCTGCCCTCCCATCTT
DNA37151	3301	CTCTCTGCCAGAGGCTCCTGGCCTGGCTGGCTGTCCCCTACCTGTGTCCCCGGCTG *****
P_AAX52256	3301	CTCTCTGCCAGAGGCTCCTGGCCTGGCTGGCTGTCCCCTACCTGTGTCCCCGGCTG
DNA37151	3361	CACCCCTCCTTCTCTTCTGTACAGTCTCAGTTGCTGTCTTGCTCCTGGCT *****
P_AAX52256	3361	CACCCCTCCTTCTCTTCTGTACAGTCTCAGTTGCTGTCTTGCTCCTGGCT *****
DNA37151	3421	CAAGGGCTGAAGGAGGCCACTCCATCTCACCTCGGGGGCTGCCCTCAATGTGGAGTGA *****
P_AAX52256	3421	CAAGGGCTGAAGGAGGCCACTCCATCTCACCTCGGGGGCTGCCCTCAATGTGGAGTGA
DNA37151	3481	CCCCAGCCAGATCTGAAGGACATTGGAGAGGGATGCCAGGAACGCCCATCTCAGCA *****
P_AAX52256	3481	CCCCAGCCAGATCTGAAGGACATTGGAGAGGGATGCCAGGAACGCCCATCTCAGCA
DNA37151	3541	GCCTGGGCTCGGCATTCCGAAGCTGACTTTCTATAGGCAATTGTACCTTGTGGAGAA *****
P_AAX52256	3541	GCCTGGGCTCGGCATTCCGAAGCTGACTTTCTATAGGCAATTGTACCTTGTGGAGAA
DNA37151	3601	ATGTGTCAACCTCCCCAACCGATTCACTCTTTCTCCTGTTGTAAAAATAAAATA *****

BLAST RESULTS A-Q

P_AAX52256 3601 ATGTGTCACCTCCCCAACCGATTCACTCTTTCTCCTGTTGTAAAAAATAAAAATA
 DNA37151 3661 AATAATAACAATAAAAAAA

 P_AAX52256 3661 AATAATAACAATAAAAAAA

>3 AC021462 Homo sapiens clone RP11-276C1, WORKING DRAFT SEQUENCE, 21 unordered (153023 bp) [1 seg]
 Score = 3658 (7251 bits), Expect = 0.0
 Identities = 3670/3674 (99%), at 1,129821-3674,133494, Strand +/-

DNA37151 1 AAGGAGGCCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTCTGGG

 AC021462 129821 AAGGAGGCCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTCTGGG
 DNA37151 61 CTCAGAAGGACTCTGAAGATAACAATAATTTCAGCCCATCCACTCTCCTCCCTCCCAA

 AC021462 129881 CTCAGAAGGACTCTGAAGATAACAATAATTTCAGCCCATCCACTCTCCTCCCTCCCAA
 DNA37151 121 CACACATGTGCATGTACACACACACACATACACACACATACACCTTCCTCTCCTTCAC TGAA

 AC021462 129941 CACACATGTGCATGTACACACACACACATACACACACATACACCTTCCTCTCCTTCAC TGAA
 DNA37151 181 GACTCACAGTCACTCACTCTGTGAGCAGGTCA TAGAAAAGGACACTAAAGCCTTAAGGAC

 AC021462 130001 GACTCACAGTCACTCACTCTGTGAGCAGGTCA TAGAAAAGGACACTAAAGCCTTAAGGAC
 DNA37151 241 AGGCCTGCCATTACCTCTGCAGCCTTGGCTTGAGTCAAAAACATGGGAGGGGG

 AC021462 130061 AGGCCTGCCATTACCTCTGCAGCCTTGGCTTGAGTCAAAAACATGGGAGGGGG
 DNA37151 301 CCAGGCACGGTGACTCACACCTGTAATCCCAGCATTTGGGAGACCAGGAGGTGAGCAGATC

 AC021462 130121 CCAGGCACGGTGACTCACACCTGTAATCCCAGCATTTGGGAGACCAGGAGGTGAGCAGATC
 DNA37151 361 ACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGGAGAAACCCCATCTCTACTA

 AC021462 130181 ACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGGAGAAACCCCATCTCTACTA
 DNA37151 421 AAAATACAAAAATTAGCCAGGAGTGGTGGCAGGTGCCTGTAATCCCAGCTACTCAGGTGG

 AC021462 130241 AAAATACAAAAATTAGCCAGGAGTGGTGGCAGGTGCCTGTAATCCCAGCTACTCAGGTGG
 DNA37151 481 CTGAGCCAGGAGAATCGCTTGAATCCAGGAGGCGGAGGATGCAGTCAGCTGAGTGCACCG

 AC021462 130301 CTGAGCCAGGAGAATCGCTTGAATCCAGGAGGCGGAGGATGCAGTCAGCTGAGTGCACCG
 DNA37151 541 CTGCACTCCAGCCTGGGTGACAGAAATGAGACTCTGCTCTCAAACAAACAAACACGGGAGGA

 AC021462 130361 CTGCACTCCAGCCTGGGTGACAGAAATGAGACTCTGCTCTCAAACAAACAAACACGGGAGGA
 DNA37151 601 GGGGTAGATACTGCTCTGCAACCTCTTAACTCTGCATCCTCTTCCAGGGCTGC

 AC021462 130421 GGGGTAGATACTGCTCTGCAACCTCTTAACTCTGCATCCTCTTCCAGGGCTGC
 DNA37151 661 CCCTGATGGGCCTGGCAATGACTGAGCAGGCCAGCCCCAGAGGAAGAGAAG

 AC021462 130481 CCCTGATGGGCCTGGCAATGACTGAGCAGGCCAGCCCCAGAGGAAGAGAAG
 DNA37151 721 CATATTGAGGAGGGCAAGAAGTGA CGCCCGGTGAGAATGACTGCCCTGGGAGGGTGGTT

 AC021462 130541 CATATTGAGGAGGGCAAGAAGTGA CGCCCGGTGAGAATGACTGCCCTGGGAGGGTGGTT
 DNA37151 781 CCTTGGCCCTGGCAGGGTTGCTGACCCTTACCGTCAAAACACAAAGAGCAGGACTCCA

BLAST RESULTS A-10

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*****
AC021462 130601 CCTTGGGCCCTGGCAGGGTTGCTGACCCCTAACCTGCAAAACACAAAGAGCAGGACTCCA
DNA37151     841 GACTCTCCTTGTGAATGGTCCCCTGCCCTGCAGCTCCACCATGAGGCTTCTCGTGGCCCC
***** ****
AC021462 130661 GACTCTTCTTGTGAATGGTCCCCTGCCCTGCAGCTCCACCATGAGGCTTCTCGTGGCCCC
DNA37151     901 ACTCTTGCTAGCTTGGGTGGCTGGTGCACACTGCCACTGTGCCGTGGTACCCCTGGCATGT
***** ****
AC021462 130721 ACTCTTGCTAGCTTGGGTGGCTGGTGCACACTGCCGTGTGCCGTGGTACCCCTGGCATGT
DNA37151     961 TCCCTGCCCTTCAGTGTGCCAGATCCGGCCCTGGTATACGCCCGCTCGTCCCTA
***** ****
AC021462 130781 TCCCTGCCCTTCAGTGTGCCAGATCCGGCCCTGGTATACGCCCGCTCGTCCCTA
DNA37151     1021 CCGCGAGGCTACCACTGTGGACTGCAATGACCTATTCTGACGGCAGTCCCCCGGCACT
***** ****
AC021462 130841 CCGCGAGGCTACCACTGTGGACTGCAATGACCTATTCTGACGGCAGTCCCCCGGCACT
DNA37151     1081 CCCCGCAGGCACACAGACCCCTGCTCCTGCAGAGCAACAGCATTGTCGTGGACCAAGAG
***** ****
AC021462 130901 CCCCGCAGGCACACAGACCCCTGCTCCTGCAGAGCAACAGCATTGTCGTGGACCAAGAG
DNA37151     1141 TGAGCTGGCTACCTGGCAATCTCACAGAGCTGGACCTGTCCCAGAACAGCTTTCGGA
***** ****
AC021462 130961 TGAGCTGGCTACCTGGCAATCTCACAGAGCTGGACCTGTCCCAGAACAGCTTTCGGA
DNA37151     1201 TGCCCGAGACTGTGATTCCATGCCCTGCCAGCTGCTGAGGCTGCACCTAGAGGAGAA
***** ****
AC021462 131021 TGCCCGAGACTGTGATTCCATGCCCTGCCAGCTGCTGAGGCTGCACCTAGAGGAGAA
DNA37151     1261 CCAGCTGACCCGGCTGGAGGACCACAGCTTGCAGGGCTGGCAGCCTACAGGAACCTCA
***** ****
AC021462 131081 CCAGCTGACCCGGCTGGAGGACCACAGCTTGCAGGGCTGGCAGCCTACAGGAACCTCA
DNA37151     1321 TCTCAACCACAACCAGCTTACCGCATGCCCTCAGGGCCTTCTGCCCTCAGCAACTT
***** ****
AC021462 131141 TCTCAACCACAACCAGCTTACCGCATGCCCTCAGGGCCTTCTGCCCTCAGCAACTT
DNA37151     1381 GCTGCGGCTGCACCTCAACTCCAACCTCCTGAGGGCATTGACAGCCGTGGTTGAAAT
***** ****
AC021462 131201 GCTGCGGCTGCACCTCAACTCCAACCTCCTGAGGGCATTGACAGCCGTGGTTGAAAT
DNA37151     1441 GCTGCCCAACTTGGAGATACTCATGATTGGCGCAACAAGGTAGATGCCATCCTGGACAT
***** ****
AC021462 131261 GCTGCCCAACTTGGAGATACTCATGATTGGCGCAACAAGGTAGATGCCATCCTGGACAT
DNA37151     1501 GAACTTCCGGCCCTGGCCAACCTGCGTAGCCTGGTGCTAGCAGGCATGAACCTGCCGGGA
***** ****
AC021462 131321 GAACTTCCGGCCCTGGCCAACCTGCGTAGCCTGGTGCTAGCAGGCATGAACCTGCCGGGA
DNA37151     1561 GATCTCCGACTATGCCCTGGAGGGCTGCAAAGCCTGGAGAGCCTCTCCTTATGACAA
***** ****
AC021462 131381 GATCTCCGACTATGCCCTGGAGGGCTGCAAAGCCTGGAGAGCCTCTCCTTATGACAA
DNA37151     1621 CCAGCTGGCCCGGGTGCCAGGCGGGCACTGGAACAGGTGCCGGCTCAAGTTCCCTAGA
***** ****
AC021462 131441 CCAGCTGGCCCGGGTGCCAGGCGGGCACTGGAACAGGTGCCGGCTCAAGTTCCCTAGA
DNA37151     1681 CCTCAACAAAGAACCCGCTCCAGCGGGTAGGGCGGGGACTTGCACATGCTGCACCT
***** ****
AC021462 131501 CCTCAACAAAGAACCCGCTCCAGCGGGTAGGGCGGGGACTTGCACATGCTGCACCT
DNA37151     1741 TAAGGAGCTGGGACTGAACAAACATGGAGGAGCTGGTCTCCATCGACAAGTTGCCCTGGT
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BEAST RESULTS A II

AC021462	131561	***** TAAGGAGCTGGGACTGAACAAACATGGAGGAGCTGGTCTCCATCGACAAGTTGCCCTGGT
DNA37151	1801	***** GAACCTCCCCGAGCTGACCAAGCTGGACATCACCAATAACCCACGGCTGCCTTCATCCA
AC021462	131621	***** GAACCTCCCCGAGCTGACCAAGCTGGACATCACCAATAACCCACGGCTGCCTTCATCCA
DNA37151	1861	***** CCCCCGCGCCTTCCACCACCTGCCCGAGATGGAGACCCCTCATGCTCAACAACAAACGCTCT
AC021462	131681	***** CCCCCGCGCCTTCCACCACCTGCCCGAGATGGAGACCCCTCATGCTCAACAACAAACGCTCT
DNA37151	1921	***** CAGTGCCTTGCACCAGCAGACGGTGGAGTCCCTGCCAACCTGCAGGAGGTAGGTCTCCA
AC021462	131741	***** CAGTGCCTTGCACCAGCAGACGGTGGAGTCCCTGCCAACCTGCAGGAGGTAGGTCTCCA
DNA37151	1981	***** CGGCAACCCCATCCGCTGTGACTGTGTCATCCGCTGGGCAATGCCACGGGCACCCGTGT
AC021462	131801	***** CGGCAACCCCATCCGCTGTGACTGTGTCATCCGCTGGGCAATGCCACGGGCACCCGTGT
DNA37151	2041	***** CCGCTTCATCGAGCCGCAATCCACCCCTGTGTCGGAGCCTCCAGCGCCTCCCC
AC021462	131861	***** CCGCTTCATCGAGCCGCAATCCACCCCTGTGTCGGAGCCTCCAGCGCCTCCCC
DNA37151	2101	***** GGTCCGTGAGGTGCCCTCCGGGAGATGACGGACCACTGTTGCCCTCATCTCCCCACG
AC021462	131921	***** GGTCCGTGAGGTGCCCTCCGGGAGATGACGGACCACTGTTGCCCTCATCTCCCCACG
DNA37151	2161	***** AAGCTTCCCCCAAGCCTCCAGGTAGCCAGTGGAGAGAGCATGGTGCTGCATTGCCGGGC
AC021462	131981	***** AAGCTTCCCCCAAGCCTCCAGGTAGCCAGTGGAGAGAGCATGGTGCTGCATTGCCGGGC
DNA37151	2221	***** ACTGGCGAACCGAACCCGAGATCTACTGGGTCACTCCAGCTGGGCTTCGACTGACACC
AC021462	132041	***** ACTGGCGAACCGAACCCGAGATCTACTGGGTCACTCCAGCTGGGCTTCGACTGACACC
DNA37151	2281	***** TGCCCATGCAGGCAGGAGGTACCGGGTGTACCCCGAGGGGACCCCTGGAGCTGGAGGGT
AC021462	132101	***** TGCCCATGCAGGCAGGAGGTACCGGGTGTACCCCGAGGGGACCCCTGGAGCTGGAGGGT
DNA37151	2341	***** GACAGCAGAAGAGGCAGGGCTATACACCTGTGTCGGCCCAGAACCTGGTGGGGCTGACAC
AC021462	132161	***** GACAGCAGAAGAGGCAGGGCTATACACCTGTGTCGGCCCAGAACCTGGTGGGGCTGACAC
DNA37151	2401	***** TAAGACGGTTAGTGTGGTTGTGGCCGTGCTCTCCTCCAGCCAGGAGGGACGAAGGACA
AC021462	132221	***** TAAGACGGTTAGTGTGGTTGTGGCCGTGCTCTCCTCCAGCCAGGAGGGACGAAGGACA
DNA37151	2461	***** GGGGCTGGAGCTCCGGGTGCAGGAGACCCACCCCTATCACATCCTGCTATCTGGGTAC
AC021462	132281	***** GGGGCTGGAGCTCCGGGTGCAGGAGACCCACCCCTATCACATCCTGCTATCTGGGTAC
DNA37151	2521	***** CCCACCCAACACAGTGTCCACCAACCTCACCTGGTCAGTGCCTCCTCCCTCGGGGCCA
AC021462	132341	***** CCCACCCAACACAGTGTCCACCAACCTCACCTGGTCAGTGCCTCCTCCCTCGGGGCCA
DNA37151	2581	***** GGGGGCCACAGCTGGCCCGCCTGCCTCGGGAACCCACAGCTACAACATTACCGCCT
AC021462	132401	***** GGGGGCCACAGCTGGCCCGCCTGCCTCGGGAACCCACAGCTACAACATTACCGCCT
DNA37151	2641	***** CCTTCAGGCCACGGAGTACTGGGCTGCCTGCAAGTGGCCTTGCTGATGCCACACCCA
AC021462	132461	***** CCTTCAGGCCACGGAGTACTGGGCTGCCTGCAAGTGGCCTTGCTGATGCCACACCCA
DNA37151	2701	***** GTTGGCTTGTGTATGGCCAGGACCAAAGAGGCCACTTCTGCCACAGAGCCTAGGGGA

BLAST RESULTS A-12

AC021462	132521	GTTGGCTTGTATGGGCCAGGACAAAGAGGCCACTTCTTGCACAGAGCCTTAGGGGA
DNA37151	2761	TCGTCCCTGGCTCATGCCATCCTGGCTCGCTGCCTCTCCCTGGCAGCTGGCTAGC
AC021462	132581	CCGTCCCTGGCTCATGCCATCCTGGCTCGCTGCCTCTCCCTGGCAGCTGGCTAGC
DNA37151	2821	GGCCCACCTTGGCACAGGCCAACCCAGGAAGGGTGTGGGTGGGAGGCAGCTCCCTCC
AC021462	132641	GGCCCACCTTGGCACAGGCCAACCCAGGAAGGGTGTGGGTGGGAGGCAGCTCCCTCC
DNA37151	2881	AGCCTGGGCTTCTGGGCTGGAGTGCCCCCTCTGTCCGGGTGTGTCTGCTCCCCCTCGT
AC021462	132701	AGCCTGGGCTTCTGGGCTGGAGTGCCCCCTCTGTCCGGGTGTGTCTGCTCCCCCTCGT
DNA37151	2941	CCTGCCCTGGAATCCAGGGAGGAAGCTGCCAGATCCTCAGAAGGGAGACACTGTTGCC
AC021462	132761	CCTGCCCTGGAATCCAGGGAGGAAGCTGCCAGATCCTCAGAAGGGAGACACTGTTGCC
DNA37151	3001	ACCATTGTCTCAAAATTCTTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGA
AC021462	132821	ACCATTGTCTCAAAATTCTTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGA
DNA37151	3061	CTACTTTTACCAAAAGAGAAGCAGTCTGGGCCAGATGCCCTGCCAGGAAAGGGACATGG
AC021462	132881	CTACTTTTACCAAAAGAGAAGCAGTCTGGGCCAGATGCCCTGCCAGGAAAGGGACATGG
DNA37151	3121	ACCCACGTGCTTGAGGCCTGGCAGCTGGCCAAGACAGATGGGCTTGTGGCCCTGGGG
AC021462	132941	ACCCACGTGCTTGAGGCCTGGCAGCTGGCCAAGACAGATGGGCTTGTGGCCCTGGGG
DNA37151	3181	TGCTTCTGCAGCCTTGAAAAGTTGCCCTACCTCCTAGGGTCACCTCTGCTGCCATTC
AC021462	133001	TGCTTCTGCAGCCTCGAAAAGTTGCCCTACCTCCTAGGGTCACCTCTGCTGCCATTC
DNA37151	3241	TGAGGAACATCTCAAGGAACAGGAGGGACTTGGCTAGAGCCTCTGCCCTCCCCTT
AC021462	133061	TGAGGAACATCTCAAGGAACAGGAGGGACTTGGCTAGAGCCTCTGCCCTCCCCTT
DNA37151	3301	CTCTCTGCCAGAGGCTCCTGGCCTGGCTTGCTGCCCTACCTGTGTCCCCGGCTG
AC021462	133121	CTCTCTGCCAGAGGCTCCTGGCCTGGCTTGCTGCCCTACCTGTGTCCCCGGCTG
DNA37151	3361	CACCCCTCCTCTTCTCTGTACAGTCTCAGTTGCTTGCTCTGTGCCCTCTGGG
AC021462	133181	CACCCCTCCTCTTCTCTGTACAGTCTCAGTTGCTTGCTCTGTGCCCTCTGGG
DNA37151	3421	CAAGGGCTGAAGGAGGCCACTCCATCTCACCTCGGGGGCTGCCCTCAATGTGGAGTGA
AC021462	133241	CAAGGGCTGAAGGAGGCCACTCCATCTCACCTCGGGGGCTGCCCTCAATGTGGAGTGA
DNA37151	3481	CCCCAGCCAGATCTGAAGGACATTGGAGAGGGATGCCAGGAACGCCATCTCAGCA
AC021462	133301	CCCCAGCCAGATCTGAAGGACATTGGAGAGGGATGCCAGGAACGCCATCTCAGCA
DNA37151	3541	GCCTGGGCTCGCATTCCGAAGCTGACTTCTATAGGCAATTGTACCTTGTGGAGAA
AC021462	133361	GCCTGGGCTCGCATTCCGAAGCTGACTTCTATAGGCAATTGTACCTTGTGGAGAA
DNA37151	3601	ATGTGTCAACCTCCCCAACCGATTCACTCTTCTCCTGTTGTAAAAATAAAAATA
AC021462	133421	ATGTGTCAACCTCCCCAACCGATTCACTCTTCTCCTGTTGTAAAAATAAAAATA
DNA37151	3661	AATAATAACAATAA

Blast results A-13

AC021462 133481 AATAATAACAATAA

>4 AL512306 Homo sapiens chromosome 1 clone RP11-430C7, *** SEQUENCING IN
(185048 bp) [1 seg]
Score = 3658 (7251 bits), Expect = 0.0
Identities = 3670/3674 (99%), at 1,107156-3674,103483, Strand +/-

DNA37151 1 AAGGAGGTGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTCTGGG

AL512306 107156 AAGGAGGTGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTCTGGG

DNA37151 61 CTCAGAAGGACTCTGAAGATAACAATAATTCAAGCCATCCACTCTCCTCCCTCCAAA

AL512306 107096 CTCAGAAGGACTCTGAAGATAACAATAATTCAAGCCATCCACTCTCCTCCCTCCAAA

DNA37151 121 CACACATGTGCATGTACACACACACATACACACACATACACCTTCCTCTCCTTCAC TGAA

AL512306 107036 CACACATGTGCATGTACACACACACATACACACACATACACCTTCCTCTCCTTCAC TGAA

DNA37151 181 GACTCACAGTCACTCACTCTGTGAGCAGGTCA TAGAAAAGGACACTAAAGCCTTAAGGAC

AL512306 106976 GACTCACAGTCACTCACTCTGTGAGCAGGTCA TAGAAAAGGACACTAAAGCCTTAAGGAC

DNA37151 241 AGGCCTGCCATTACCTCTGCAGCCTTGGCTTGGAGTGAGTCAAAAAACATGGGAGGGGG

AL512306 106916 AGGCCTGCCATTACCTCTGCAGCCTTGGCTTGGAGTGAGTCAAAAAACATGGGAGGGGG

DNA37151 301 CCAGGCACGGTGACTCACACCTGTAA TCCCAGCATTTGGGAGACCGAGGTGAGCAGATC

AL512306 106856 CCAGGCACGGTGACTCACACCTGTAA TCCCAGCATTTGGGAGACCGAGGTGAGCAGATC

DNA37151 361 ACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGAGAAACCCCCATCTCTACTA

AL512306 106796 ACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGAGAAACCCCCATCTCTACTA

DNA37151 421 AAAATACAAAAATTAGCCAGGAGTGGTGGCAGGTGCCTGTAA TCCCAGCTACTCAGGTGG

AL512306 106736 AAAATACAAAAATTAGCCAGGAGTGGTGGCAGGTGCCTGTAA TCCCAGCTACTCAGGTGG

DNA37151 481 CTGAGCCAGGAGAATCGCTTGAATCCAGGAGGCGGAGGATGCAGTCAGCTGAGTGCACCG

AL512306 106676 CTGAGCCAGGAGAATCGCTTGAATCCAGGAGGCGGAGGATGCAGTCAGCTGAGTGCACCG

DNA37151 541 CTGCACTCCAGCCTGGGTGACAGAATGAGACTCTGTCTCAAACAAACAAACACGGGAGGA

AL512306 106616 CTGCACTCCAGCCTGGGTGACAGAATGAGACTCTGTCTCAAACAAACAAACACGGGAGGA

DNA37151 601 GGGGTAGATACTGCTCTGTCAACCTCTTAACTCTGCATCCTCTTCCAGGGCTGC

AL512306 106556 GGGGTAGATACTGCTCTGTCAACCTCTTAACTCTGCATCCTCTTCCAGGGCTGC

DNA37151 661 CCCTGATGGGCCTGGCAATGACTGAGCAGGCCAGCCCCAGAGGACAAGGAAGAGAAGG

AL512306 106496 CCCTGATGGGCCTGGCAATGACTGAGCAGGCCAGCCCCAGAGGACAAGGAAGAGAAGG

DNA37151 721 CATATTGAGGAGGGCAAGAAGTGA CGCCCGGTGAGAATGACTGCCCTGGGAGGGTGGTT

AL512306 106436 CATATTGAGGAGGGCAAGAAGTGA CGCCCGGTGAGAATGACTGCCCTGGGAGGGTGGTT

DNA37151 781 CCTTGGGCCTGGCAGGGTTGCTGACCTTACCCCTGCAAAACACAAAGAGCAGGACTCCA

AL512306 106376 CCTTGGGCCTGGCAGGGTTGCTGACCTTACCCCTGCAAAACACAAAGAGCAGGACTCCA

DNA37151	841	GAECTCTCCTTGTGAATGGTCCCTGCCCTGCAGCTCCACCATGAGGCTCTCGTGGCCCC *****
AL512306	106316	GAECTCTCCTTGTGAATGGTCCCTGCCCTGCAGCTCCACCATGAGGCTCTCGTGGCCCC
DNA37151	901	ACTCTTGCTAGCTGGTGGCTGGTGCCTGCAGCTCCACATGTGCCGTGGTACCCCTGGCATGT *****
AL512306	106256	ACTCTTGCTAGCTGGTGGCTGGTGCCTGCAGCTCCACATGTGCCGTGGTACCCCTGGCATGT
DNA37151	961	TCCCTGCCCCCTCAGTGTGCCTGCCAGATCCGGCCCTGGTATACGCCCGCTCGTCCTA *****
AL512306	106196	TCCCTGCCCCCTCAGTGTGCCTGCCAGATCCGGCCCTGGTATACGCCCGCTCGTCCTA
DNA37151	1021	CCCGAGGCTACCACTGTGGACTGCAATGACCTATTCCGTGACGGCAGTCCCCCGGCACT *****
AL512306	106136	CCCGAGGCTACCACTGTGGACTGCAATGACCTATTCCGTGACGGCAGTCCCCCGGCACT
DNA37151	1081	CCCCGCAGGCACACAGACCCCTGCCTGCAGAGCAACAGCATGTCCGTGGACCAGAG *****
AL512306	106076	CCCCGCAGGCACACAGACCCCTGCCTGCAGAGCAACAGCATGTCCGTGGACCAGAG
DNA37151	1141	TGAGCTGGCTACCTGGCCAATCTCACAGAGCTGGACCTGTCCCAGAACAGCTTTCGGA *****
AL512306	106016	TGAGCTGGCTACCTGGCCAATCTCACAGAGCTGGACCTGTCCCAGAACAGCTTTCGGA
DNA37151	1201	TGCCCAGACTGTGATTCCATGCCCTGCCAGCTGCTGAGGCTGCACCTAGAGGAGAA *****
AL512306	105956	TGCCCAGACTGTGATTCCATGCCCTGCCAGCTGCTGAGGCTGCACCTAGAGGAGAA
DNA37151	1261	CCAGCTGACCCGGCTGGAGGACACAGCTTGCAGGGCTGGCAGCCTACAGGAACCTA *****
AL512306	105896	CCAGCTGACCCGGCTGGAGGACACAGCTTGCAGGGCTGGCAGCCTACAGGAACCTA
DNA37151	1321	TCTCAACCACAACCAGCTTACCGCATGCCCTGCCAGGGCCTTTCTGGCCTCAGCAACTT *****
AL512306	105836	TCTCAACCACAACCAGCTTACCGCATGCCCTGCCAGGGCCTTTCTGGCCTCAGCAACTT
DNA37151	1381	GCTGCGGCTGCACCTCAACTCCAACCTCCTGAGGGCATTGACAGCCGCTGGTTGAAAT *****
AL512306	105776	GCTGCGGCTGCACCTCAACTCCAACCTCCTGAGGGCATTGACAGCCGCTGGTTGAAAT
DNA37151	1441	GCTGCCCAACTGGAGATACTCATGATTGGCGAACAGGTAGATGCCATCCTGGACAT *****
AL512306	105716	GCTGCCCAACTGGAGATACTCATGATTGGCGAACAGGTAGATGCCATCCTGGACAT
DNA37151	1501	GAACCTCCGGCCCTGGCAACCTGCCTAGCCTGGCTAGCAGGCATGAACCTGCGGGA *****
AL512306	105656	GAACCTCCGGCCCTGGCAACCTGCCTAGCCTGGCTAGCAGGCATGAACCTGCGGGA
DNA37151	1561	GATCTCCGACTATGCCCTGGAGGGCTGCAAAGCCTGGAGAGCCTCTCCTTATGACAA *****
AL512306	105596	GATCTCCGACTATGCCCTGGAGGGCTGCAAAGCCTGGAGAGCCTCTCCTTATGACAA
DNA37151	1621	CCAGCTGGCCGGGTGCCAGGGCAACTGGAACAGGTGCCGGCTCAAGTTCTAGA *****
AL512306	105536	CCAGCTGGCCGGGTGCCAGGGCAACTGGAACAGGTGCCGGCTCAAGTTCTAGA
DNA37151	1681	CCTCAACAAGAACCCGCTCCAGCGGGTAGGGCCGGGGACTTGCCAACATGCTGCACCT *****
AL512306	105476	CCTCAACAAGAACCCGCTCCAGCGGGTAGGGCCGGGGACTTGCCAACATGCTGCACCT
DNA37151	1741	TAAGGAGCTGGGACTGAACAACATGGAGGAGCTGGTCTCCATGACAAGTTGCCCTGGT *****
AL512306	105416	TAAGGAGCTGGGACTGAACAACATGGAGGAGCTGGTCTCCATGACAAGTTGCCCTGGT

BLAST RESULTS A-15

DNA37151	1801	GAACCTCCCCGAGCTGACCAAGCTGGACATCACCAATAACCCACGGCTGCCTTCATCCA *****
AL512306	105356	GAACCTCCCCGAGCTGACCAAGCTGGACATCACCAATAACCCACGGCTGCCTTCATCCA *****
DNA37151	1861	CCCCCGGCCCTTCCACCACCTGCCCGAGATGGAGACCCCTCATGCTCAACAACAACGCTCT *****
AL512306	105296	CCCCCGGCCCTTCCACCACCTGCCCGAGATGGAGACCCCTCATGCTCAACAACAACGCTCT *****
DNA37151	1921	CAGTGCCTTGCACCAGCAGACGGTGGAGTCCCTGCCAACCTGCAGGAGGTAGGTCTCCA *****
AL512306	105236	CAGTGCCTTGCACCAGCAGACGGTGGAGTCCCTGCCAACCTGCAGGAGGTAGGTCTCCA *****
DNA37151	1981	CGGCAACCCCATTCCGCTGTGACTGTGTCATCCGCTGGGCCAATGCCACGGCACCCGTGT *****
AL512306	105176	CGGCAACCCCATTCCGCTGTGACTGTGTCATCCGCTGGGCCAATGCCACGGCACCCGTGT *****
DNA37151	2041	CCGCTTCATCGAGCCGCAATCCACCCCTGTGCGGAGCCTCCGGACCTCCAGCGCCTCCC *****
AL512306	105116	CCGCTTCATCGAGCCGCAATCCACCCCTGTGCGGAGCCTCCGGACCTCCAGCGCCTCCC *****
DNA37151	2101	GGTCCGTGAGGTGCCCTTCCGGGAGATGACGGACCACTGTTGCCCTCATCTCCCCACG *****
AL512306	105056	GGTCCGTGAGGTGCCCTTCCGGGAGATGACGGACCACTGTTGCCCTCATCTCCCCACG *****
DNA37151	2161	AAGCTTCCCCCAAGCCTCCAGGTAGCCAGTGGAGAGAGCATGGTGCTGCATTGCCGGC *****
AL512306	104996	AAGCTTCCCCCAAGCCTCCAGGTAGCCAGTGGAGAGAGCATGGTGCTGCATTGCCGGC *****
DNA37151	2221	ACTGGCCGAACCGAACCCGAGATCTACTGGGTCACTCCAGCTGGGTTTCGACTGACACC *****
AL512306	104936	ACTGGCCGAACCGAACCCGAGATCTACTGGGTCACTCCAGCTGGGTTTCGACTGACACC *****
DNA37151	2281	TGCCCATGCAGGCAGGAGGTACCGGGTGTACCCCGAGGGGACCCCTGGAGCTGCGGAGGGT *****
AL512306	104876	TGCCCATGCAGGCAGGAGGTACCGGGTGTACCCCGAGGGGACCCCTGGAGCTGCGGAGGGT *****
DNA37151	2341	GACAGCAGAAGAGGCAGGGCTATACACCTGTGTCGCCAGAACCTGGTGGGGCTGACAC *****
AL512306	104816	GACAGCAGAAGAGGCAGGGCTATACACCTGTGTCGCCAGAACCTGGTGGGGCTGACAC *****
DNA37151	2401	TAAGACGGTTAGTGTGGTTGTGGCGTGTCTCCTCCAGCCAGGCAGGGACGAAGGACA *****
AL512306	104756	TAAGACGGTTAGTGTGGTTGTGGCGTGTCTCCTCCAGCCAGGCAGGGACGAAGGACA *****
DNA37151	2461	GGGGCTGGAGCTCCGGGTGCAGGAGACCCACCCCTATCACATCCTGCTATCTGGTCAC *****
AL512306	104696	GGGGCTGGAGCTCCGGGTGCAGGAGACCCACCCCTATCACATCCTGCTATCTGGTCAC *****
DNA37151	2521	CCCACCCAACACAGTGTCCACCAACCTCACCTGGTCAGTGCCTCCTCCCTCGGGGCCA *****
AL512306	104636	CCCACCCAACACAGTGTCCACCAACCTCACCTGGTCAGTGCCTCCTCCCTCGGGGCCA *****
DNA37151	2581	GGGGGCCACAGCTTGGCCCGCCTGCCCTGGGAACCCACAGCTACAACATTACCCGCC *****
AL512306	104576	GGGGGCCACAGCTTGGCCCGCCTGCCCTGGGAACCCACAGCTACAACATTACCCGCC *****
DNA37151	2641	CCTTCAGGCCACGGAGTACTGGGCCTGCCGTCAAGTGGCCTTGCTGATGCCACACCCA *****
AL512306	104516	CCTTCAGGCCACGGAGTACTGGGCCTGCCGTCAAGTGGCCTTGCTGATGCCACACCCA *****
DNA37151	2701	GTTGGCTTGTGTATGGGCCAGGACCAAAGAGGCCACTTCTTGCCACAGGCCCTAGGGGA *****
AL512306	104456	GTTGGCTTGTGTATGGGCCAGGACCAAAGAGGCCACTTCTTGCCACAGGCCCTAGGGGA *****

BLAST RESULTS A-10

DNA37151	2761	TCGTCCCTGGCTCATGCCATCCTGGCTCGCTGCCTCTCCCTGGCAGCTGGCTAGC *****
AL512306	104396	CCGTCCCTGGCTCATGCCATCCTGGCTCGCTGCCTCTCCCTGGCAGCTGGCTAGC
DNA37151	2821	GGCCCACCTTGGCACAGGCCAACCCAGGAAGGGTGTGGGTGGGAGGCAGGCCTCTCC *****
AL512306	104336	GGCCCACCTTGGCACAGGCCAACCCAGGAAGGGTGTGGGTGGGAGGCAGGCCTCTCC *****
DNA37151	2881	AGCCTGGGCTTCTGGGCTGGAGTGCCCCCTCTGTCCGGTTGTGTCTGCTCCCCTCGT *****
AL512306	104276	AGCCTGGGCTTCTGGGCTGGAGTGCCCCCTCTGTCCGGTTGTGTCTGCTCCCCTCGT
DNA37151	2941	CCTGCCCTGGAATCCAGGGAGGAAGCTGCCAGATCCTCAGAAGGGAGACACTGTTGCC *****
AL512306	104216	CCTGCCCTGGAATCCAGGGAGGAAGCTGCCAGATCCTCAGAAGGGAGACACTGTTGCC
DNA37151	3001	ACCATTGTCTCAAAATTCTTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGA *****
AL512306	104156	ACCATTGTCTCAAAATTCTTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGA
DNA37151	3061	CTACTTTTACCAAAAGAGAAGCAGTCTGGGCCAGATGCCCTGCCAGGAAAGGGACATGG *****
AL512306	104096	CTACTTTTACCAAAAGAGAAGCAGTCTGGGCCAGATGCCCTGCCAGGAAAGGGACATGG
DNA37151	3121	ACCCACGTGCTTGAGGCCTGGCAGCTGGCCAAGACAGATGGGGTTGTGGCCCTGGGG *****
AL512306	104036	ACCCACGTGCTTGAGGCCTGGCAGCTGGCCAAGACAGATGGGGTTGTGGCCCTGGGG
DNA37151	3181	GTGCTTCTGCAGCCTTGAAAAGTTGCCCTTACCTCCTAGGGTCACCTCTGCTGCCATT *****
AL512306	103976	GTGCTTCTGCAGCCTCGAAAAGTTGCCCTTACCTCCTAGGGTCACCTCTGCTGCCATT
DNA37151	3241	TGAGGAACATCTCAAGGAACAGGAGGGACTTGGCTAGAGCCTCCTGCCCTCCCCATCTT *****
AL512306	103916	TGAGGAACATCTCAAGGAACAGGAGGGACTTGGCTAGAGCCTCCTGCCCTCCCCATCTT
DNA37151	3301	CTCTCTGCCAGAGGCTCCTGGCCTGGCTGGCTGTCCCCTACCTGTGTCCCCGGGCTG *****
AL512306	103856	CTCTCTGCCAGAGGCTCCTGGCCTGGCTGGCTGTCCCCTACCTGTGTCCCCGGGCTG
DNA37151	3361	CACCCCTTCCTCTTCTCTGTACAGTCTCAGTTGCTTGTGCCTCGGCCCTGGG *****
AL512306	103796	CACCCCTTCCTCTTCTCTGTACAGTCTCAGTTGCTTGTGCCTCGGCCCTGGG
DNA37151	3421	CAAGGGCTGAAGGAGGCCACTCCATCTCACCTCGGGGGCTGCCCTCAATGTGGAGTGA *****
AL512306	103736	CAAGGGCTGAAGGAGGCCACTCCATCTCACCTCGGGGGCTGCCCTCAATGTGGAGTGA
DNA37151	3481	CCCCAGCCAGATCTGAAGGACATTGGAGAGGGATGCCAGGAACGCCCTCATCTCAGCA *****
AL512306	103676	CCCCAGCCAGATCTGAAGGACATTGGAGAGGGATGCCAGGAACGCCCTCATCTCAGCA
DNA37151	3541	GCCTGGGCTCGGCATTCCGAAGCTGACTTTCTATAGGCAATTGTACCTTGTGGAGAA *****
AL512306	103616	GCCTGGGCTCGGCATTCCGAAGCTGACTTTCTATAGGCAATTGTACCTTGTGGAGAA
DNA37151	3601	ATGTGTCACCTCCCCAACCGATTCACTCTTCTCCTGTTGTAAAAATAAAAATA *****
AL512306	103556	ATGTGTCACCTCCCCAACCGATTCACTCTTCTCCTGTTGTAAAAATAAAAATA
DNA37151	3661	AATAATAACAATAA *****
AL512306	103496	AATAATAACAATAA

BLAST RESULTS A-17

>5 NM_006338 Homo sapiens glioma amplified on chromosome 1 protein (3227 bp) [1 seg]

Score = 3002 (5951 bits), Expect = 0.0

Identities = 3017/3022 (99%), at 653,161-3674,3182, Strand +/+

DNA37151	653	AGGGCTGCCCTGATGGGCCTGGCAATGACTGAGCAGGCCAGCCCCAGAGGACAAGGA *****
NM_006338	161	AGGGCTGCCCTGATGGGCCTGGCAATGACTGAGCAGGCCAGCCCCAGAGGACAAGGA *****
DNA37151	713	AGAGAAGGCATATTGAGGAGGGCAAGAACAGTACGCCGGTGTAGAACATGACTGCCCTGGGA *****
NM_006338	221	AGAGAAGGCATATTGAGGAGGGCAAGAACAGTACGCCGGTGTAGAACATGACTGCCCTGGGA *****
DNA37151	773	GGGTGGTTCCCTGGGCCTGGCAGGGTTGCTGACCTTACCTGCAAAACACAAAGAGCA *****
NM_006338	281	GGGTGGTTCCCTGGGCCTGGCAGGGTTGCTGACCTTACCTGCAAAACACAAAGAGCA *****
DNA37151	833	GGACTCCAGACTCTCCTGTGAATGGTCCCCTGCCCTGCAGCTCACCATGAGGCTTCTC *****
NM_006338	341	GGACTCCAGACTCTCCTGTGAATGGTCCCCTGCCCTGCAGCTCACCATGAGGCTTCTC *****
DNA37151	893	GTGGCCCCACTCTGCTAGCTGGGTGGCTGGCCACTGCCACTGTGCCGTGGTACCC *****
NM_006338	401	GTGGCCCCACTCTGCTAGCTGGGTGGCTGGCCACTGCCGTGTGCCGTGGTACCC *****
DNA37151	953	TGGCATTTCCCTGCCCTCAGTGTGCCCTGCCAGATCCGGCCCTGGTACGCCCGC *****
NM_006338	461	TGGCATTTCCCTGCCCTCAGTGTGCCCTGCCAGATCCGGCCCTGGTACGCCCGC *****
DNA37151	1013	TCGTCCCTACCGCGAGGCTACCACTGTGGACTGCAATGACCTATTCTGACGGCAGTCCCC *****
NM_006338	521	TCGTCCCTACCGCGAGGCTACCACTGTGGACTGCAATGACCTATTCTGACGGCAGTCCCC *****
DNA37151	1073	CCGGCACTCCCCGCAAGCACACAGACCCCTGCTCCTGCAGAGAACAGCATTGTCCGTGTG *****
NM_006338	581	CCGGCACTCCCCGCAAGCACACAGACCCCTGCTCCTGCAGAGAACAGCATTGTCCGTGTG *****
DNA37151	1133	GACCAGAGTGAGCTGGCTACCTGGCAATCTCACAGAGCTGGACCTGTCCAGAACAGC *****
NM_006338	641	GACCAGAGTGAGCTGGCTACCTGGCAATCTCACAGAGCTGGACCTGTCCAGAACAGC *****
DNA37151	1193	TTTCGGATGCCGAGACTGTGATTCCATGCCCTGGCCAGCTGCTGAGCCTGCACCTA *****
NM_006338	701	TTTCGGATGCCGAGACTGTGATTCCATGCCCTGGCCAGCTGCTGAGCCTGCACCTA *****
DNA37151	1253	GAGGAGAACAGCTGACCCGGCTGGAGGACACAGCTTGCAAGGGCTGGCCAGCCTACAG *****
NM_006338	761	GAGGAGAACAGCTGACCCGGCTGGAGGACACAGCTTGCAAGGGCTGGCCAGCCTACAG *****
DNA37151	1313	GAACCTATCTCAACCACAAACCAAGCTACCGCATGCCCTGGCCAGGGCTTTCTGGCCTC *****
NM_006338	821	GAACCTATCTCAACCACAAACCAAGCTACCGCATGCCCTGGCCAGGGCTTTCTGGCCTC *****
DNA37151	1373	AGCAACTTGCTGCCGCTGCACCTCAACTCCAACCTCTGAGGGCATTGACAGCCGCTGG *****
NM_006338	881	AGCAACTTGCTGCCGCTGCACCTCAACTCCAACCTCTGAGGGCATTGACAGCCGCTGG *****
DNA37151	1433	TTTGAAATGCTGCCAACCTGGAGATACTCATGATTGGCGGCAACAAGGTAGATGCCATC *****
NM_006338	941	TTTGAAATGCTGCCAACCTGGAGATACTCATGATTGGCGGCAACAAGGTAGATGCCATC *****
DNA37151	1493	CTGGACATGAACCTCCGGCCCTGGCAACCTGCGTAGCCTGGCTAGCAGGCATGAAC *****
NM_006338	1001	CTGGACATGAACCTCCGGCCCTGGCAACCTGCGTAGCCTGGCTAGCAGGCATGAAC *****

BLAST RESULTS A10

DNA37151	1553	CTGCAGGGAGATCTCCGACTATGCCCTGGAGGGGCTGCAAAGCCTGGAGAGCCTCTCCTTC
NM_006338	1061	***** CTGCAGGGAGATCTCCGACTATGCCCTGGAGGGGCTGCAAAGCCTGGAGAGCCTCTCCTTC
DNA37151	1613	TATGACAACCAGCTGGCCCGGGTGCCAGGCAGGGCACTGGAACAGGTGCCCGGGCTCAAG
NM_006338	1121	***** TATGACAACCAGCTGGCCCGGGTGCCAGGCAGGGCACTGGAACAGGTGCCCGGGCTCAAG
DNA37151	1673	TTCCCTAGACCTAACAAAGAACCCGCTCCAGCGGGTAGGGCCGGGGACTTGCCAACATG
NM_006338	1181	***** TTCCCTAGACCTAACAAAGAACCCGCTCCAGCGGGTAGGGCCGGGGACTTGCCAACATG
DNA37151	1733	CTGCACCTTAAGGAGCTGGACTGAACAAACATGGAGGAGCTGGCTCCATCGACAAGTT
NM_006338	1241	***** CTGCACCTTAAGGAGCTGGACTGAACAAACATGGAGGAGCTGGCTCCATCGACAAGTT
DNA37151	1793	GCCCTGGTGAACCTCCCCGAGCTGACCAAGCTGGACATCACCAATAACCCACGGCTGTCC
NM_006338	1301	***** GCCCTGGTGAACCTCCCCGAGCTGACCAAGCTGGACATCACCAATAACCCACGGCTGTCC
DNA37151	1853	TTCATCCACCCCCGCGCCTTCCACCACCTGCCAGATGGAGAACCTCATGCTAACAAAC
NM_006338	1361	***** TTCATCCACCCCCGCGCCTTCCACCACCTGCCAGATGGAGAACCTCATGCTAACAAAC
DNA37151	1913	AACGCTCTCAGTGCCTTGCACCAAGCAGCGTGGAGTCCCTGCCAACCTGCAGGAGGTA
NM_006338	1421	***** AACGCTCTCAGTGCCTTGCACCAAGCAGCGTGGAGTCCCTGCCAACCTGCAGGAGGTA
DNA37151	1973	GGTCTCCACGGCAACCCCATCCGCTGTGACTGTGTCATCCGCTGGCCAATGCCACGGG
NM_006338	1481	***** GGTCTCCACGGCAACCCCATCCGCTGTGACTGTGTCATCCGCTGGCCAATGCCACGGG
DNA37151	2033	ACCCGTGTCCGCTTCATCGAGCCGAATCCACCCCTGTGTGCGGAGCCTCCGGACCTCCAG
NM_006338	1541	***** ACCCGTGTCCGCTTCATCGAGCCGAATCCACCCCTGTGTGCGGAGCCTCCGGACCTCCAG
DNA37151	2093	CGCCTCCCGTCCGTGAGGTGCCCTTCCGGGAGATGACGGACCACTGTTGCCCTCATC
NM_006338	1601	***** CGCCTCCCGTCCGTGAGGTGCCCTTCCGGGAGATGACGGACCACTGTTGCCCTCATC
DNA37151	2153	TCCCCACGAAGCTCCCCCAAGCCTCCAGGTAGCCAGTGGAGAGAGCATGGTGTGCTGCAT
NM_006338	1661	***** TCCCCACGAAGCTCCCCCAAGCCTCCAGGTAGCCAGTGGAGAGAGCATGGTGTGCTGCAT
DNA37151	2213	TGCCGGGCACTGGCGAACCGAACCCGAGATCTACTGGTCACTCCAGCTGGCTTCGA
NM_006338	1721	***** TGCCGGGCACTGGCGAACCGAACCCGAGATCTACTGGTCACTCCAGCTGGCTTCGA
DNA37151	2273	CTGACACCTGCCATGCAGGCAGGAGGTACCGGGTGTACCCGAGGGACCTGGAGCTG
NM_006338	1781	***** CTGACACCTGCCATGCAGGCAGGAGGTGCCGGGTGTACCCGAGGGACCTGGAGCTG
DNA37151	2333	CGGAGGGTGACAGCAGAAGAGGCAGGGCTATACACCTGTGTGGCCCAGAACCTGGTGGGG
NM_006338	1841	***** CGGAGGGTGACAGCAGAAGAGGCAGGGCTATACACCTGTGTGGCCCAGAACCTGGTGGGG
DNA37151	2393	GCTGACACTAACAGACGGTTAGTGTGGTTGTGGCCGTGCTCTCCAGCCAGGCAGGGAC
NM_006338	1901	***** GCTGACACTAACAGACGGTTAGTGTGGTTGTGGCCGTGCTCTCCAGCCAGGCAGGGAC
DNA37151	2453	GAAGGACAGGGGCTGGAGCTCCGGGTGCAGGAGACCCACCCCTATCACATCCTGCTATCT
NM_006338	1961	***** GAAGGACAGGGGCTGGAGCTCCGGGTGCAGGAGACCCACCCCTATCACATCCTGCTATCT

BLAST RESULTS A19

DNA37151	2513	TGGGTACCCCCACCAACACAGTGTCCACCAACCTCACCTGGTCCAGTGCCTCCTCCCTC *****
NM_006338	2021	TGGGTACCCCCACCAACACAGTGTCCACCAACCTCACCTGGTCCAGTGCCTCCTCCCTC *****
DNA37151	2573	CGGGGCCAGGGGCCACAGCTCTGGCCCGCCTGCCTCGGGAAACCCACAGCTACAACATT *****
NM_006338	2081	CGGGGCCAGGGGCCACAGCTCTGGCCCGCCTGCCTCGGGAAACCCACAGCTACAACATT *****
DNA37151	2633	ACCCGCCTCCTTCAGGCCACGGAGTACTGGGCCTGCCTGCAAGTGGCCTTGCTGATGCC *****
NM_006338	2141	ACCCGCCTCCTTCAGGCCACGGAGTACTGGGCCTGCCTGCAAGTGGCCTTGCTGATGCC *****
DNA37151	2693	CACACCCAGTTGGCTTGTATGGGCCAGGACAAAGAGGCCACTTCTGCCACAGAGCC *****
NM_006338	2201	CACACCCAGTTGGCTTGTATGGGCCAGGACAAAGAGGCCACTTCTGCCACAGAGCC *****
DNA37151	2753	TTAGGGGATCGCCTGGCTCATGCCATCCTGGCTCTGCTGTCCCTCCTGGCAGCT *****
NM_006338	2261	TTAGGGGATCGCCTGGCTCATGCCATCCTGGCTCTGCTGTCCCTCCTGGCAGCT *****
DNA37151	2813	GGGCTAGCGCCCACCTTGGCACAGGCCAACCCAGGAAGGGTGTGGTGGAGGCGCCT *****
NM_006338	2321	GGGCTAGCGCCCACCTTGGCACAGGCCAACCCAGGAAGGGTGTGGTGGAGGCGCCT *****
DNA37151	2873	CTCCCTCCAGCCTGGCTTCTGGAGTGCCTCTGGCTCTGTCCTGGGTTGTCTGCT *****
NM_006338	2381	CTCCCTCCAGCCTGGCTTCTGGAGTGCCTCTGGCTCTGTCCTGGGTTGTCTGCT *****
DNA37151	2933	CCCCTCGCCTGCCCTGGAATCCAGGGAGGAAGCTGCCAGATCCTCAGAAGGGGAGACA *****
NM_006338	2441	CCCCTCGCCTGCCCTGGAATCCAGGGAGGAAGCTGCCAGATCCTCAGAAGGGGAGACA *****
DNA37151	2993	CTGTTGCCACCATTGTCTAAAATTCTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAAT *****
NM_006338	2501	CTGTTGCCACCATTGTCTAAAATTCTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAAT *****
DNA37151	3053	CACTAGGACTACTTTTACCAAAAGAGAAGCAGTCTGGGCCAGATGCCCTGCCAGGAAAG *****
NM_006338	2561	CACTAGGACTACTTTTACCAAAAGAGAAGCAGTCTGGGCCAGATGCCCTGCCAGGAAAG *****
DNA37151	3113	GGACATGGACCCACGTGCTTGAGGCCTGGCAGCTGGCCAAGACAGATGGGCTTTGTGG *****
NM_006338	2621	GGACATGGACCCACGTGCTTGAGGCCTGGCAGCTGGCCAAGACAGATGGGCTTTGTGG *****
DNA37151	3173	CCCTGGGGGTGCTCTGCAGCCTGAAAAAGTTGCCCTTACCTCCTAGGGTCACCTCTGC *****
NM_006338	2681	CCCTGGGGGTGCTCTGCAGCCTGAAAAAGTTGCCCTTACCTCCTAGGGTCACCTCTGC *****
DNA37151	3233	TGCCATTCTGAGGAACATCTCAAGGAACAGGAGGGACTTGGCTAGAGCCTCCTGCCTC *****
NM_006338	2741	TGCCATTCTGAGGAACATCTCAAGGAACAGGAGGGACTTGGCTAGAGCCTCCTGCCTC *****
DNA37151	3293	CCCATCTCTCTGCCAGAGGCTCCTGGCCTGGCTGGCTGTCCCCTACCTGTGTCC *****
NM_006338	2801	CCCATCTCTCTGCCAGAGGCTCCTGGCCTGGCTGTCCCCTACCTGTGTCC *****
DNA37151	3353	CCGGGCTGCACCCCTTCCTCTTCTCTGTACAGTCTCAGTTGCTTGCTCTGTGC *****
NM_006338	2861	CCGGGCTGCACCCCTTCCTCTTCTCTGTACAGTCTCAGTTGCTTGCTCTGTGC *****
DNA37151	3413	CTCCTGGGCAAGGGCTGAAGGAGGCCACTCCATCTCACCTCGGGGGCTGCCCTCAATGT *****
NM_006338	2921	CTCCTGGGCAAGGGCTGAAGGAGGCCACTCCATCTCACCTCGGGGGCTGCCCTCAATGT *****

BLAST RESULTS Ar20

DNA37151	3473	GGGAGTACCCAGCCAGATCTGAAGGACATTGGAGAGGGATGCCAGGAACGCCTCA *****
NM_006338	2981	GGGAGTACCCAGCCAGATCTGAAGGACATTGGAGAGGGATGCCAGGAACGCCTCA *****
DNA37151	3533	TCTCAGCAGCCTGGGCTCGGCATTCCGAAGCTGACTTCTATAAGCAATTGTACCTTT *****
NM_006338	3041	TCTCAGCAGCCTGGGCTCGGCATTCCGAAGCTGACTTCTATAAGCAATTGTACCTTT *****
DNA37151	3593	GTGGAGAAATGTGTACCTCCCCAACCGATTCACTTTCTCTGTGGTAAAAAA *****
NM_006338	3101	GTGGAGAAATGTGTACCTCCCCAACCGATTCACTTTCTCTGTGGTAAAAAA *****
DNA37151	3653	TAAAAATAATAACAATAA *****
NM_006338	3161	TAAAAATAATAACAATAA *****

>6 AF030435 Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA (3227 bp) [1 seg]
Score = 3002 (5951 bits), Expect = 0.0
Identities = 3017/3022 (99%), at 653,161-3674,3182, Strand +/+

DNA37151	653	AGGGCTGCCCTGATGGGGCTGGCAATGACTGAGCAGGCCAGCCCCAGAGGACAAGGA *****
AF030435	161	AGGGCTGCCCTGATGGGGCTGGCAATGACTGAGCAGGCCAGCCCCAGAGGACAAGGA *****
DNA37151	713	AGAGAAGGCATATTGAGGAGGGCAAGAAGTGACGCCGGTGTAGAATGACTGCCCTGGGA *****
AF030435	221	AGAGAAGGCATATTGAGGAGGGCAAGAAGTGACGCCGGTGTAGAATGACTGCCCTGGGA *****
DNA37151	773	GGGTGGTCCTGGCCCTGGCAGGGTTGCTGACCTTACCTGAAAACACAAAGAGCA *****
AF030435	281	GGGTGGTCCTGGCCCTGGCAGGGTTGCTGACCTTACCTGAAAACACAAAGAGCA *****
DNA37151	833	GGACTCCAGACTCTCCTGTGAATGGTCCCCTGCCCTGCAGCTCCACCATGAGGCTTCTC *****
AF030435	341	GGACTCCAGACTCTCCTGTGAATGGTCCCCTGCCCTGCAGCTCCACCATGAGGCTTCTC *****
DNA37151	893	GTGGCCCCACTTTGCTAGCTGGTGGCTGGCACTGCCACTGTGCCGTGGTACCC *****
AF030435	401	GTGGCCCCACTTTGCTAGCTGGTGGCTGGCACTGCCGTGTGCCGTGGTACCC *****
DNA37151	953	TGGCATGTTCCCTGCCCTCAGTGTGCCAGATCCGGCCCTGGTACGCCCTGGC *****
AF030435	461	TGGCATGTTCCCTGCCCTCAGTGTGCCAGATCCGGCCCTGGTACGCCCTGGC *****
DNA37151	1013	TCGTCTACCGCGAGGCTACCACTGTGGACTGCAATGACCTATTCTGACGGCAGTCCCC *****
AF030435	521	TCGTCTACCGCGAGGCTACCACTGTGGACTGCAATGACCTATTCTGACGGCAGTCCCC *****
DNA37151	1073	CCGGCACTCCCCGCAGGCACACAGACCTGCTCCTGCAGAGCAACAGCATTGTCCGTGTG *****
AF030435	581	CCGGCACTCCCCGCAGGCACACAGACCTGCTCCTGCAGAGCAACAGCATTGTCCGTGTG *****
DNA37151	1133	GACCAGAGTGAGCTGGCTACCTGGCAATCTCACAGAGCTGGACCTGTCCAGAACAGC *****
AF030435	641	GACCAGAGTGAGCTGGCTACCTGGCAATCTCACAGAGCTGGACCTGTCCAGAACAGC *****
DNA37151	1193	TTTCGGATGCCAGAGACTGTGATTCCATGCCCTGCCAGCTGCTGAGCCTGCACCTA *****
AF030435	701	TTTCGGATGCCAGAGACTGTGATTCCATGCCCTCCCCAGCTGCTGAGCCTGCACCTA *****
DNA37151	1253	GAGGAGAACAGCTGACCCGGCTGGAGGACACAGCTTGCAAGGGCTGGCCAGCCTACAG *****

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AF030435	761	GAGGAGAACAGCTGACCCGGCTGGAGGACCACAGCTTGACGGCTGGCAGCCTACAG
DNA37151	1313	GAACTCTATCTCAACCACAACCAGCTTACCGCATCGCCCCAGGGCTTTCTGGCTC *****
AF030435	821	GAACTCTATCTCAACCACAACCAGCTTACCGCATCGCCCCAGGGCTTTCTGGCTC
DNA37151	1373	AGCAACTTGCTGCCAACTTGAGATACTCATGATTGGCGAACAAAGGTAGATGCCATC *****
AF030435	881	AGCAACTTGCTGCCAACTTGAGATACTCATGATTGGCGAACAAAGGTAGATGCCATC
DNA37151	1433	TTTGAATGCTGCCAACTTGAGATACTCATGATTGGCGAACAAAGGTAGATGCCATC *****
AF030435	941	TTTGAATGCTGCCAACTTGAGATACTCATGATTGGCGAACAAAGGTAGATGCCATC
DNA37151	1493	CTGGACATGAACCTCCGGCCCTGGCCAACCTCGTAGCCTGGTCTAGCAGGCATGAAC *****
AF030435	1001	CTGGACATGAACCTCCGGCCCTGGCCAACCTCGTAGCCTGGTCTAGCAGGCATGAAC
DNA37151	1553	CTGCGGGAGATCTCGACTATGCCCTGGAGGGCTGCAAAGCCTGGAGAGCCTCTCCTTC *****
AF030435	1061	CTGCGGGAGATCTCGACTATGCCCTGGAGGGCTGCAAAGCCTGGAGAGCCTCTCCTTC
DNA37151	1613	TATGACAACCAGCTGGCCGGTGCCAGGCGGGCACTGGAACAGGTGCCCGGGCTCAAG *****
AF030435	1121	TATGACAACCAGCTGGCCGGTGCCAGGCGGGCACTGGAACAGGTGCCCGGGCTCAAG
DNA37151	1673	TTCCTAGACCTAACAGAACCCGCTCCAGCGGGTAGGGCCGGGACTTTGCCAACATG *****
AF030435	1181	TTCCTAGACCTAACAGAACCCGCTCCAGCGGGTAGGGCCGGGACTTTGCCAACATG
DNA37151	1733	CTGCACCTTAAGGAGCTGGACTGAACAAACATGGAGGAGCTGGTCTCCATCGACAAGTT *****
AF030435	1241	CTGCACCTTAAGGAGCTGGACTGAACAAACATGGAGGAGCTGGTCTCCATCGACAAGTT
DNA37151	1793	GCCCTGGTGAACCTCCCCGAGCTGACCAAGCTGGACATCACCAATAACCCACGGCTGTCC *****
AF030435	1301	GCCCTGGTGAACCTCCCCGAGCTGACCAAGCTGGACATCACCAATAACCCACGGCTGTCC
DNA37151	1853	TTCATCCACCCCGCGCCTTCACCACTGCCAGATGGAGACCCCTATGCTAACAAAC *****
AF030435	1361	TTCATCCACCCCGCGCCTTCACCACTGCCAGATGGAGACCCCTATGCTAACAAAC
DNA37151	1913	AACGCTCTCAGTGCCTTGACCCAGCAGACGGTGGAGTCCCTGCCAACCTGCAGGAGGTA *****
AF030435	1421	AACGCTCTCAGTGCCTTGACCCAGCAGACGGTGGAGTCCCTGCCAACCTGCAGGAGGTA
DNA37151	1973	GGTCTCCACGGCAACCCCATCCGCTGTGACTGTGTCATCCGCTGGCCAATGCCACGGGC *****
AF030435	1481	GGTCTCCACGGCAACCCCATCCGCTGTGACTGTGTCATCCGCTGGCCAATGCCACGGGC
DNA37151	2033	ACCCGTGTCCGTTCATCGAGCCGAATCCACCCCTGTGTGCGGAGCCTCCGGACCTCCAG *****
AF030435	1541	ACCCGTGTCCGTTCATCGAGCCGAATCCACCCCTGTGTGCGGAGCCTCCGGACCTCCAG
DNA37151	2093	CGCCTCCCGTCCGTGAGGTGCCCTCCGGGAGATGACGGACCACTGTTGCCCTCATC *****
AF030435	1601	CGCCTCCCGTCCGTGAGGTGCCCTCCGGGAGATGACGGACCACTGTTGCCCTCATC
DNA37151	2153	TCCCCACGAAGCTCCCCCAAGCCTCCAGGTAGCCAGTGGAGAGAGCATGGTGTGCTGCAT *****
AF030435	1661	TCCCCACGAAGCTCCCCCAAGCCTCCAGGTAGCCAGTGGAGAGAGCATGGTGTGCTGCAT
DNA37151	2213	TGCCGGGACTGGCCGAACCCGAACCGAGATCTACTGGGTCACTCCAGCTGGCTTCGA *****

BLAST RESULTS 4-22

AF030435	1721	TGCCGGGCACTGGCCGAACCGAACCCGAGATCTACTGGGTCACTCCAGCTGGCTTCGA *****
DNA37151	2273	CTGACACCTGCCATGCAGGCAGGAGTACCGGGTGTACCCCGAGGGGACCCCTGGAGCTG *****
AF030435	1781	CTGACACCTGCCATGCAGGCAGGAGTGCAGGGTGTACCCCGAGGGGACCCCTGGAGCTG *****
DNA37151	2333	CGGAGGGTGACAGCAGAAGAGGCAGGGCTATACACCTGTGTGCCAGAACCTGGTGGGG *****
AF030435	1841	CGGAGGGTGACAGCAGAAGAGGCAGGGCTATACACCTGTGTGCCAGAACCTGGTGGGG *****
DNA37151	2393	GCTGACACTAAAGACGGTTAGTGTGGTTGTGGCCGTGCTCTCCTCCAGCAGGCAGGGAC *****
AF030435	1901	GCTGACACTAAAGACGGTTAGTGTGGTTGTGGCCGTGCTCTCCTCCAGCAGGCAGGGAC *****
DNA37151	2453	GAAGGACAGGGCTGGAGCTCCGGGTGCAGGAGACCCACCCCTATCACATCCTGCTATCT *****
AF030435	1961	GAAGGACAGGGCTGGAGCTCCGGGTGCAGGAGACCCACCCCTATCACATCCTGCTATCT *****
DNA37151	2513	TGGGTACCCCCACCCAACACAGTGTCCACCAACCTCACCTGGTCCAGTGCCTCCTCCCTC *****
AF030435	2021	TGGGTACCCCCACCCAACACAGTGTCCACCAACCTCACCTGGTCCAGTGCCTCCTCCCTC *****
DNA37151	2573	CGGGGCCAGGGGCCACAGCTCTGGCCCGCCTGCCTCGGGAAACCCACAGCTACAACATT *****
AF030435	2081	CGGGGCCAGGGGCCACAGCTCTGGCCCGCCTGCCTCGGGAAACCCACAGCTACAACATT *****
DNA37151	2633	ACCCGCCTCCTCAGGCCACGGAGTACTGGGCCTGCCTGCAAGTGGCTTGCTGATGCC *****
AF030435	2141	ACCCGCCTCCTCAGGCCACGGAGTACTGGGCCTGCCTGCAAGTGGCTTGCTGATGCC *****
DNA37151	2693	CACACCCAGTTGGCTTGTGTATGGGCAGGACCAAAGAGGCCACTTCTGCCACAGAGCC *****
AF030435	2201	CACACCCAGTTGGCTTGTGTATGGGCAGGACCAAAGAGGCCACTTCTGCCACAGAGCC *****
DNA37151	2753	TTAGGGGATCGCCTGGCTCATGCCATCCTGGCTCTGCTGTCTTCCTGGCAGCT *****
AF030435	2261	TTAGGGGATCGCCTGGCTCATGCCATCCTGGCTCTGCTGTCTTCCTGGCAGCT *****
DNA37151	2813	GGGCTAGCGGCCACCTTGGCACAGGCCAACCCAGGAAGGGTGTGGTGGGAGGCGCCT *****
AF030435	2321	GGGCTAGCGGCCACCTTGGCACAGGCCAACCCAGGAAGGGTGTGGTGGGAGGCGCCT *****
DNA37151	2873	CTCCCTCCAGCCTGGCTTCTGGGCTGGAGTGCCCCTCTGTCCGGTTGTCTGCT *****
AF030435	2381	CTCCCTCCAGCCTGGCTTCTGGGCTGGAGTGCCCCTCTGTCCGGTTGTCTGCT *****
DNA37151	2933	CCCCTCGCCTGCCCTGGAATCCAGGGAGGAAGCTGCCAGATCCTCAGAACGGGAGACA *****
AF030435	2441	CCCCTCGCCTGCCCTGGAATCCAGGGAGGAAGCTGCCAGATCCTCAGAACGGGAGACA *****
DNA37151	2993	CTGTTGCCACCATTGTCTCAAAATTCTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAAT *****
AF030435	2501	CTGTTGCCACCATTGTCTCAAAATTCTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAAT *****
DNA37151	3053	CACTAGGACTACTTTTACCAAAAGAGAACAGTCAGTCTGGGCCAGATGCCCTGCCAGGAAAG *****
AF030435	2561	CACTAGGACTACTTTTACCAAAAGAGAACAGTCAGTCTGGGCCAGATGCCCTGCCAGGAAAG *****
DNA37151	3113	GGACATGGACCCACGTGCTTGAGGCCTGGCAGCTGGCCAAGACAGATGGGCTTGTGG *****
AF030435	2621	GGACATGGACCCACGTGCTTGAGGCCTGGCAGCTGGCCAAGACAGATGGGCTTGTGG *****
DNA37151	3173	CCCTGGGGTGCTTCTGCAGCCTTGAAAAAGTTGCCCTACCTCCTAGGGTCACCTCTGC *****

BLAST RESULTS Ar-23

AF030435	2681	CCCTGGGGTGCTTCTGCAGCCTGAAAAAGTTGCCCTACCTCCTAGGGTCACCTCTGC
DNA37151	3233	TGCCATTCTGAGGAACATCTCCAAGGAACAGGAGGGACTTTGGCTAGAGCCTCCTGCCCTC *****
AF030435	2741	TGCCATTCTGAGGAACATCTCCAAGGAACGGGAAGGGACTTTGGCTAGAGCCTCCTGCCCTC
DNA37151	3293	CCCATCTCTCTGCCAGAGGCTCCTGGCCTGGCTGTCCCCTACCTGTGTCC *****
AF030435	2801	CCCATCTCTCTGCCAGAGGCTCCTGGCCTGGCTGTCCCCTACCTGTGTCC
DNA37151	3353	CCGGGCTGCACCCCTTCCTCTCTCTGTACAGTCTCAGTTGCTGCTCTGTGC *****
AF030435	2861	CCGGGCTGCACCCCTTCCTCTCTGTACAGTCTCAGTTGCTGCTCTGTGC
DNA37151	3413	CTCCTGGCAAGGGCTGAAGGAGGCCACTCCATCTCACCTCGGGGGCTGCCCTCAATGT *****
AF030435	2921	CTCCTGGCAAGGGCTGAAGGAGGCCACTCCATCTCACCTCGGGGGCTGCCCTCAATGT
DNA37151	3473	GGGAGTGACCCCAGCCAGATCTGAAGGACATTGGGAGAGGGATGCCAGGAACGCCCTCA *****
AF030435	2981	GGGAGTGACCCCAGCCAGATCTGAAGGACATTGGGAGAGGGATGCCAGGAACGCCCTCA
DNA37151	3533	TCTCAGCAGCCTGGCTCGGCATTCCGAAGCTGACTTTCTATAGGCAATTGTACCTTT *****
AF030435	3041	TCTCAGCAGCCTGGCTCGGCATTCCGAAGCTGACTTTCTATAGGCAATTGTACCTTT
DNA37151	3593	GTGGAGAAATGTGTACACCTCCCCAACCGATTCACTCTTCTCCTGTTGTAAAAAA *****
AF030435	3101	GTGGAGAAATGTGTACACCTCCCCAACCGATTCACTCTTCTCCTGTTGTAAAAAA
DNA37151	3653	AAAAAATAATAATAACAATAAA *****
AF030435	3161	AAAAAATAATAATAACAATAAA

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(B)

Tue Jul 17 13:25:00 2001 [BLASTP 2.1.3 [Apr-1-2001], APR 05 2002
/home/ruby/va/Molbio/carpenda/temp1/p1.DNA37151 (713 aa)

TECH CENTER 1600/2900

BLAST RESULTS B-1

Sequences producing High-scoring Segment Pairs:

		Score	Match	Pct	E-val
1	P_AAB80253 Human PRO293 protein - Homo sapiens.	3732	713	100	0.0
2	P_AAY13385 protein PRO293 - Homo sapiens.	3732	713	100	0.0
3	NP_006329.1 glioma amplified on chromosome 1 protein (3718	711	100	0.0
4	GAC1_HUMAN Glioma amplified on chromosome 1 protein p	3718	711	100	0.0

>1 P_AAB80253 Human PRO293 protein - Homo sapiens. (713 aa) [1 seg]

Score = 3732 (1442 bits), Expect = 0.0

Identities = 713/713 (100%), Positives = 713/713 (100%), at 1,1-713,713

DNA37151	1	MRLLVAPLLLAWVAGATATVPVVPHVPCPPQCACQIRPWYTPRSSYREATTVDNDLFL	*****
P_AAB80253	1	MRLLVAPLLLAWVAGATATVPVVPHVPCPPQCACQIRPWYTPRSSYREATTVDNDLFL	*****
DNA37151	61	TAVPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARCDFHALPQLL	*****
P_AAB80253	61	TAVPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARCDFHALPQLL	*****
DNA37151	121	SLHLEENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAI	*****
P_AAB80253	121	SLHLEENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAI	*****
DNA37151	181	DSRFWFEMLPNLEILMIGGNKVDAILDMDNFRPLANLRSVLAGMNLREISDYALEGLQSL	*****
P_AAB80253	181	DSRFWFEMLPNLEILMIGGNKVDAILDMDNFRPLANLRSVLAGMNLREISDYALEGLQSL	*****
DNA37151	241	SLSFYDNQLARVPRRALEQVPGLKFLDLNKNPLQRVPGDFANMLHLKELGLNNMEELVS	*****
P_AAB80253	241	SLSFYDNQLARVPRRALEQVPGLKFLDLNKNPLQRVPGDFANMLHLKELGLNNMEELVS	*****
DNA37151	301	IDKFALVNLPELTKLDTNNPRLSFIHPRAFHLPQMETLMLNNNALSALHQQTVESLPN	*****
P_AAB80253	301	IDKFALVNLPELTKLDTNNPRLSFIHPRAFHLPQMETLMLNNNALSALHQQTVESLPN	*****
DNA37151	361	LQEVLGHGNPIRCDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHC	*****
P_AAB80253	361	LQEVLGHGNPIRCDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHC	*****
DNA37151	421	LPLISPRSFPPLQVASGESMVLHCRALAEPPEPEIYWVTPAGLRLTPAHAGRRYRVPEG	*****
P_AAB80253	421	LPLISPRSFPPLQVASGESMVLHCRALAEPPEPEIYWVTPAGLRLTPAHAGRRYRVPEG	*****
DNA37151	481	TLELRRVTAAEAGLYTCVAQNLVGADTKTVSVVGRALLQPGRDEGQGLELRVQETHPYH	*****
P_AAB80253	481	TLELRRVTAAEAGLYTCVAQNLVGADTKTVSVVGRALLQPGRDEGQGLELRVQETHPYH	*****
DNA37151	541	ILLSWVTPPNTVSTNLTWSSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVA	*****
P_AAB80253	541	ILLSWVTPPNTVSTNLTWSSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVA	*****
DNA37151	601	FADAHTQLACVWARTKEATSCHRALGDRPGLIAILALAVLLAAGLAHLGTGQPRKGVG	*****
P_AAB80253	601	FADAHTQLACVWARTKEATSCHRALGDRPGLIAILALAVLLAAGLAHLGTGQPRKGVG	*****

DNA37151 661 GRRPLPPAWFWGSAPSVRVSAPLVPWNPGRLPRSSGETLLPPLSQNS

P_AAB80253 661 GRRPLPPAWFWGSAPSVRVSAPLVPWNPGRLPRSSGETLLPPLSQNS

>2 P_AAY13385 protein PRO293 - Homo sapiens. (713 aa) [1 seg]
Score = 3732 (1442 bits), Expect = 0.0
Identities = 713/713 (100%), Positives = 713/713 (100%), at 1,1-713,713

DNA37151 1 MRLLVAPILLLAWVAGATATVPVVPHVPCPPQCACQIRPWYTPRSSYREATTVDNDLFL

P_AAY13385 1 MRLLVAPILLLAWVAGATATVPVVPHVPCPPQCACQIRPWYTPRSSYREATTVDNDLFL

DNA37151 61 TAVPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLL

P_AAY13385 61 TAVPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLL

DNA37151 121 SLHLEENQLTRLEDHSFAGLASLQEELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAI

P_AAY13385 121 SLHLEENQLTRLEDHSFAGLASLQEELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAI

DNA37151 181 DSRWFEMLPNLEILMIGGNKVDAILDMDNFRPLANLRSVLVAGMNLREISDYALEGLQSL

P_AAY13385 181 DSRWFEMLPNLEILMIGGNKVDAILDMDNFRPLANLRSVLVAGMNLREISDYALEGLQSL

DNA37151 241 SLSFYDNQLARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVS

P_AAY13385 241 SLSFYDNQLARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVS

DNA37151 301 IDKFALVNLPELTKLDTNNPRLSFIHPRAFHLPQMETLMLNNNALSALHQQTVESLPN

P_AAY13385 301 IDKFALVNLPELTKLDTNNPRLSFIHPRAFHLPQMETLMLNNNALSALHQQTVESLPN

DNA37151 361 LQEVLGHGNPIRCDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHC

P_AAY13385 361 LQEVLGHGNPIRCDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHC

DNA37151 421 LPLISPRSFPPLSQLVQASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEG

P_AAY13385 421 LPLISPRSFPPLSQLVQASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEG

DNA37151 481 TLELRRVTAAEAGLYTCVAQNLVGADTKTVSVVGRALLQPGRDEGQGLELRVQETHPYH

P_AAY13385 481 TLELRRVTAAEAGLYTCVAQNLVGADTKTVSVVGRALLQPGRDEGQGLELRVQETHPYH

DNA37151 541 ILLSWVTPPNTVSTNLTWSSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVA

P_AAY13385 541 ILLSWVTPPNTVSTNLTWSSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVA

DNA37151 601 FADAHTQLACVWARTKEATSCHRALGDRGLIAILALAVLLAAGLAHLGTGQPRKGVG

P_AAY13385 601 FADAHTQLACVWARTKEATSCHRALGDRGLIAILALAVLLAAGLAHLGTGQPRKGVG

DNA37151 661 GRRPLPPAWFWGSAPSVRVSAPLVPWNPGRLPRSSGETLLPPLSQNS

P_AAY13385 661 GRRPLPPAWFWGSAPSVRVSAPLVPWNPGRLPRSSGETLLPPLSQNS

BLAST RESULTS B-3

>3 NP_006329.1 glioma amplified on chromosome 1 protein (leucine-rich) - Homo (713 aa) [1 seg]

Score = 3718 (1436 bits), Expect = 0.0

Identities = 711/713 (99%), Positives = 711/713 (99%), at 1,1-713, 713

DNA37151	1	MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFL *****
NP_006329.1	1	MRLLVAPLLLAWVAGATAAVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFL
DNA37151	61	TAVPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLL *****
NP_006329.1	61	TAVPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLL
DNA37151	121	SLHLEENQLTRLEDHSFAGLASLQEELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAI *****
NP_006329.1	121	SLHLEENQLTRLEDHSFAGLASLQEELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAI
DNA37151	181	DSRFWFEMLPNLEILMIGGNKVDAILDMNFRPLANLRSVLVAGMNLREISDYALEGLQSL *****
NP_006329.1	181	DSRFWFEMLPNLEILMIGGNKVDAILDMNFRPLANLRSVLVAGMNLREISDYALEGLQSL
DNA37151	241	SLSFYDNQLARVPRALEQVPGLKFLDLNKNPLQRVPGDFANMLHLKELGLNNMEELVS *****
NP_006329.1	241	SLSFYDNQLARVPRALEQVPGLKFLDLNKNPLQRVPGDFANMLHLKELGLNNMEELVS
DNA37151	301	IDKFALVNLPPELTKLIDITNNPRLSFIHPRAFHHPQMETLMLNNNALSALHQQTVESLPN *****
NP_006329.1	301	IDKFALVNLPPELTKLIDITNNPRLSFIHPRAFHHPQMETLMLNNNALSALHQQTVESLPN
DNA37151	361	LQEVLGHGNPIRCDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHC *****
NP_006329.1	361	LQEVLGHGNPIRCDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHC
DNA37151	421	LPLISPRSFPPLSQLVASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVPEG *****
NP_006329.1	421	LPLISPRSFPPLSQLVASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRCRVYPEG
DNA37151	481	TLELRRVTAAEAGLYTCVAQNLVGADTKTVSVVGRALLQPGRDEGQGLELRVQETHPYH *****
NP_006329.1	481	TLELRRVTAAEAGLYTCVAQNLVGADTKTVSVVGRALLQPGRDEGQGLELRVQETHPYH
DNA37151	541	ILLSWVTPPNTVSTNLTWSSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVA *****
NP_006329.1	541	ILLSWVTPPNTVSTNLTWSSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVA
DNA37151	601	FADAHTQLACVWARTKEATSCHRALGDRPGLIAILALAVLLAAGLAAHLGTGQPRKGVG *****
NP_006329.1	601	FADAHTQLACVWARTKEATSCHRALGDRPGLIAILALAVLLAAGLAAHLGTGQPRKGVG
DNA37151	661	GRRPLPPAWFWGWSAPSVRVVSAPLVLWPWNPGRKLPRSSEGETLLPPLSQNS *****
NP_006329.1	661	GRRPLPPAWFWGWSAPSVRVVSAPLVLWPWNPGRKLPRSSEGETLLPPLSQNS

>4 GAC1_HUMAN Glioma amplified on chromosome 1 protein precursor /pid=AAC39792.1 - homo sapiens (713 aa) [1 seg]

Score = 3718 (1436 bits), Expect = 0.0

Identities = 711/713 (99%), Positives = 711/713 (99%), at 1,1-713, 713

BLAST RESULTS B-A

DNA37151	1	MRLLVAPLLLAWVAGATAATPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFL *****
GAC1_HUMAN	1	MRLLVAPLLLAWVAGATAAVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFL *****
DNA37151	61	TAVPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLL *****
GAC1_HUMAN	61	TAVPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLL *****
DNA37151	121	SLHLEENQLTRLEDHSFAGLASLQEELYLNHNQLYRIAPRAFSGLSNLLRLHLSNLLRAI *****
GAC1_HUMAN	121	SLHLEENQLTRLEDHSFAGLASLQEELYLNHNQLYRIAPRAFSGLSNLLRLHLSNLLRAI *****
DNA37151	181	DSRFWFEMLPNLEILMIGGNKVDAILDMNFRPLANLRSVLVLAGMNLREISDYALEGLQSL *****
GAC1_HUMAN	181	DSRFWFEMLPNLEILMIGGNKVDAILDMNFRPLANLRSVLVLAGMNLREISDYALEGLQSL *****
DNA37151	241	SLSFYDNQLARVPRALEQVPGLKFIDLNKNPLQRVPGDFANMLHLKELGLNNMEELVS *****
GAC1_HUMAN	241	SLSFYDNQLARVPRALEQVPGLKFIDLNKNPLQRVPGDFANMLHLKELGLNNMEELVS *****
DNA37151	301	IDKFALVNLPPELTKLIDITNNPRLSFIHPRAFHHPQMETLMLNNNALSALHQQTVESLPN *****
GAC1_HUMAN	301	IDKFALVNLPPELTKLIDITNNPRLSFIHPRAFHHPQMETLMLNNNALSALHQQTVESLPN *****
DNA37151	361	LQEVGLHGNPIRCDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHC *****
GAC1_HUMAN	361	LQEVGLHGNPIRCDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHC *****
DNA37151	421	LPLISPRSFPPLQVASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVPEG *****
GAC1_HUMAN	421	LPLISPRSFPPLQVASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRCRVPEG *****
DNA37151	481	TLELRRVTAAEAGLYTCVAQNLVGADTKTVSVVGRALLQPGRDEGQGLELRVQETHPYH *****
GAC1_HUMAN	481	TLELRRVTAAEAGLYTCVAQNLVGADTKTVSVVGRALLQPGRDEGQGLELRVQETHPYH *****
DNA37151	541	ILLSWVTPPNTVSTNLTWSSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVA *****
GAC1_HUMAN	541	ILLSWVTPPNTVSTNLTWSSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVA *****
DNA37151	601	FADAHTQLACVWARTKEATSCHRALGDRPGLIAILALAVLLAAGLAHLGTGQPRKGVG *****
GAC1_HUMAN	601	FADAHTQLACVWARTKEATSCHRALGDRPGLIAILALAVLLAAGLAHLGTGQPRKGVG *****
DNA37151	661	GRRPLPPAWFWGWSAPSVRVVSAPLVPWNPGRKLPSSSEGETLLPPLSQNS *****
GAC1_HUMAN	661	GRRPLPPAWFWGWSAPSVRVVSAPLVPWNPGRKLPSSSEGETLLPPLSQNS *****